

74617

**From:** Schultz, James  
**Sent:** Thursday, August 29, 2002 4:48 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence search for 8 cases

Hello,

I have 8 cases that all require identical sequence searches (the only variables being the SEQ ID to be searched, the length of the target, and the length of the hit returned). If it suits you, I would like to condense all requests to this email. If you prefer 8 different emails, please respond and I'll split the requests up.

For all 8 cases, I need a length limited search against each of the sequences listed below. The maximum length of each hit to be returned follows each SEQ ID.

CASE 10/019,470,	SEQ ID. NO 1, 2828 nt long,	max return hit length, 30 nucleotides
CASE 10/049,743,	SEQ ID. NO 1, 3868 nt long,	max return hit length, 30 nucleotides
CASE 10/154,708,	SEQ ID. NO 3, 1834 nt long,	max return hit length, 30 nucleotides
CASE 10/177,554	SEQ ID. NO 4, 1321 nt long,	max return hit length, 80 nucleotides
CASE 10/174,456,	SEQ ID. NO 4, 2724 nt long,	max return hit length, 80 nucleotides
CASE 10/174,128,	SEQ ID. NO 4, 755 nt long,	max return hit length, 80 nucleotides
CASE 10/189,268,	SEQ ID. NO 4, 1395 nt long,	max return hit length, 80 nucleotides
CASE 10/178,258,	SEQ ID. NO 4, 1550 nt long,	max return hit length, 80 nucleotides

Thanks, Doug

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CMI 6B02 Tel: 305-9203

AUG 30 2002  
REC'D ED  
LJ/CHM DIVISION  
(STIC)  
(3,6)

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 8/31/02  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: Q6  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 23:42:49 ; Search time 3483.49 Seconds  
(without alignments)  
16938.780 Million cell updates/sec

Title: US-10-019-470-1  
Perfect score: 2888  
Sequence: 1 qttgaaaggctctggcgccg.....aaagtgtcaatttccaaggaa 2828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 524256

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :	GenEmbl: 1: gb_ba: 2: gb_htg: 3: gb_in: 4: gb_on: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_cv: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_htg_hum: 31: em_htg_inv: 32: em_htg_other: 33: em_htg_o_inv: 				
RESULT : 1	AX096602	21 bp	DNA	linear	PAT 30-MAR-2001
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
LOCUS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
DEFINITION	1 (bases 1 to 21)				
ACCESSION	Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.				
VERSION	GR:13512856				
KEYWORDS	Single nucleotide polymorphisms in genes				
SOURCE	Patent: WO 018250 A 1780 15 MAR 2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)				
ORGANISM	Location,Qualifiers				
REFERENCE	McCarty,J.J.				
AUTHORS	JOURNAL				
TITLE	Patent				
JOURNAL	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium				
SUMMARIES	Pharmaceuticals, Inc. (US)				
FEATURES	Location,Qualifiers				
source	1. /organism="Homo sapiens" /db_xref="taxon:9606"				
BASE COUNT	6 a 7 c 3 g 4 t 1 others				
Result No.	Score	Query Match Length	DB ID	Description	
8					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ORIGIN Query Match 0.7%; Score 20.6; DB 6; Length 21; Best Local Similarity 95.2%; Pred. No. 4.8e+06; Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy / 1123 agctgaatgtatactaccctc 1143  
Db 1 AGCTGATGAACTACCCCTC 21

RESULT 2 AX096603 Locus AX096603 Sequence 1781 from Patent WO0118250.

DEFINITION Sequence 1781 from Patent WO0118250.

VERSION AX096603.1 GI:13512857

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 21)

AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.

TITLE Patent: WO 0118250-A 1781 15-MAR-2001; WHITHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)

JOURNAL Single nucleotide polymorphisms in genes

FEATURES Location/Qualifiers 1..21

SOURCE /organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 7 a 3 c 4 g 6 t 1 others

ORIGIN ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 21; Best Local Similarity 95.2%; Pred. No. 4.8e+06; Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy / 1978 agctgatcattcaagtggcag 1998  
Db 1 AGCTGATCACCTAGTGGCAG 21

RESULT 5 AX096606 Locus AX096606 Sequence 1784 from Patent WO0118250.

DEFINITION Sequence 1784 from Patent WO0118250.

VERSION AX096606.1 GI:13512860

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 21)

AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.

TITLE Patent: WO 0118250-A 1784 15-MAR-2001; WHITHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)

JOURNAL Single nucleotide polymorphisms in genes

FEATURES Location/Qualifiers 1..21

SOURCE /organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 5 a 3 c 8 g 4 t 1 others

ORIGIN ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 21; Best Local Similarity 95.2%; Pred. No. 4.8e+06; Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1377 gatgtggaccctctgagaagg 1397  
 |:|||||:|||||:|||||:  
 Db 1 GATGTGGACCCTCTGAGAGG 21

**RESULT 6**

LOCUS AX153968 Sequence 66 from Patent WO0138576. 21 bp DNA linear PAT 22-JUN-2001

DEFINITION AX153968  
 VERSION AX153968.1 GI:14535582  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 KEYWORD human.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
 TITLE Human single nucleotide polymorphisms  
 JOURNAL Patent: WO 0138576-A 68 31 MAY-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
 FEATURES source Location/Qualifiers  
 1..21 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 6 a 4 c 5 g 5 t 1 others  
 ORIGIN

Query Match Best Local Similarity 95.2%; Score 20.6; DB 6; Length 21;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

REF ID: AX153968

QY 1218 aaccagaagacctcgccata 1238  
 |||||:|||||:  
 Db 1 AACCAAAGAAGCTTCGCCATAC 21

**RESULT 7**

LOCUS AX153969 Sequence 67 from Patent WO0138576. 21 bp DNA linear PAT 22-JUN-2001

DEFINITION AX153969  
 VERSION AX153969.1 GI:14535583  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 KEYWORD human.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
 TITLE Human single nucleotide polymorphisms  
 JOURNAL Patent: WO 0138576-A 67 31 MAY-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
 FEATURES source Location/Qualifiers  
 1..21 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 4 a 7 c 6 g 3 t 1 others  
 ORIGIN

Query Match Best Local Similarity 95.2%; Score 20.6; DB 6; Length 21;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

REF ID: AX153969

QY 1706 cttccggaaactcgccaagg 1726  
 |||||:|||||:  
 Db 1 CCTCCGGAAACTCGCCAAGGT 21

**RESULT 8**

LOCUS AX153970 Sequence 68 from Patent WO0138576. 21 bp DNA linear PAT 22-JUN-2001

DEFINITION AX153970  
 VERSION AX153970  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 KEYWORD human.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
 TITLE Human single nucleotide polymorphisms  
 JOURNAL Patent: WO 0138576-A 68 31 MAY-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
 FEATURES source Location/Qualifiers  
 1..21 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 6 a 4 c 5 g 5 t 1 others  
 ORIGIN

Query Match Best Local Similarity 95.2%; Score 20.6; DB 6; Length 21;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

REF ID: AX153970

QY 2003 ggtagacaatggccatgtgt 2023  
 |||||:|||||:  
 Db 1 GGTAACAAATRACCCATTGGT 21

**RESULT 9**

LOCUS AX153971 Sequence 69 from Patent WO0138576. 21 bp DNA linear PAT 22-JUN-2001

DEFINITION AX153971  
 VERSION AX153971  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 KEYWORD human.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
 TITLE Human single nucleotide polymorphisms  
 JOURNAL Patent: WO 0138576-A 69 31 MAY-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
 FEATURES source Location/Qualifiers  
 1..21 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 4 a 7 c 7 g 2 t 1 others  
 ORIGIN

Query Match Best Local Similarity 95.2%; Score 20.6; DB 6; Length 21;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

REF ID: AX153971

QY 2119 ctgcaggcaccgaacctcg 2139  
 |||||:|||||:  
 Db 1 CTGCAGCAGCAACTCG 21



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**RESULT 15**  
**AX306690** AX306690 29 bp DNA linear PAT 11-DEC-2001  
**DEFINITION** Sequence 8 from Patent WO0187945.  
**ACCESSION** AX306690  
**VERSION** AX306690.1 GI:17645857  
**KEYWORDS**  
**SOURCE**  
**ORGANISM** synthetic construct.  
 synthetic construct.  
 artificial sequence.  
**REFERENCE** 1 (sites)  
**AUTHORS** Rosenthal,M.S., Cox,G.N. and Doherty,D.H.  
**TITLE** Methods for refolding proteins containing free cysteine residues  
**JOURNAL** Patent: WO 0187925-A 8 22-NOV-2001;  
 Bolder Biotechnology, Inc. (US)  
**FEATURES** Location/Qualifiers  
 1. 29  
 /organism="synthetic construct"  
 /db\_xref="Taxon:32630"  
 /note="primer"  
**BASE COUNT** 4 a 13 c 9 g 3 t  
**ORIGIN**

**Query Match** 0.7%; Score 19; DB 6; Length 29;  
**Best Local Similarity** 81.5%; Pred. No. 1e+07;  
**Matches** 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
**Qy** 788 gccatatgacacccccggccggcta 814  
**Db** 2 GCCATATGACCCCGCTGGGCCGCCA 28

Search completed: September 7, 2002, 02:03:23  
 Job time: 8434 sec

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Result No.	Score	Query	Match	Length	DB	ID	Description	Location/Qualifiers
1	27	1.0	27	21	AAA14004		Human liver glycogen	FT /tag= a
2	21	0.7	21	21	AAA14002		Human liver glycogen	FT /tag= b
c 3	21	0.7	21	21	AAA14003		Human liver glycogen	FT /tag= "conjugated to fluorescent reporter dye TAMRA"
c 4	21	0.7	21	22	AAH62165		Phosphorylases glyc	XX
5	21	0.7	21	22	AAH62166		Phosphorylases glyc	PN US6043091-A.
6	21	0.7	21	22	AAH62167		Phosphorylases glyc	XX
7	21	0.7	21	22	AAH62168		Phosphorylases glyc	PD .28-MAR-2000.
8	21	0.7	21	22	AAH62169		Phosphorylases glyc	XX
9	21	0.7	21	22	AAH62170		Phosphorylases glyc	PF 19-JUL-1999; 99US-0357071.

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 00:22:14 ; Search time 306.44 Seconds

(without alignments)  
15844.648 Million cell updates/secTitle: US-10-019-470-1  
Perfect score: 2828Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters:

166488

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_023802 :\*

1: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1980.DAT :\*  
 2: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1981.DAT :\*  
 3: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1982.DAT :\*  
 4: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1983.DAT :\*  
 5: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1984.DAT :\*  
 6: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1985.DAT :\*  
 7: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1986.DAT :\*  
 8: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1987.DAT :\*  
 9: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1988.DAT :\*  
 10: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1989.DAT :\*  
 11: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1990.DAT :\*  
 12: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1991.DAT :\*  
 13: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1992.DAT :\*  
 14: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1993.DAT :\*  
 15: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1994.DAT :\*  
 16: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1995.DAT :\*  
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 19: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1998.DAT :\*  
 20: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA1999.DAT :\*  
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 22: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA2001.DAT :\*  
 23: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA2001B.DAT :\*  
 24: /SIDS1/gcdata/hold-geneseq/geneseq -emb1/NA2002.DAT :\*

RESULT 1  
ID AAA14004 standard; DNA; 27 BP.  
XX AAA14004;  
XX DT 18-JUL-2000 (first entry)  
DE Human liver glycogen phosphorylase quantitative real-time PCR probe #4.  
XX AC  
XX KW Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;  
KW 1,4-alpha-D-glucan-orthophosphate alpha-D-glucosidase; HGLPA;  
KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;  
KW expression inhibition; antisense therapy; hypoglycaemic;  
KW type II diabetes; non insulin-dependent;  
KW quantitative real-time PCR probe; ss.  
XX OS Homo sapiens.  
XX FH Key modified\_base FT modified\_base FT  
XX /tag= "conjugated to fluorescent reporter dye TAMRA"

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	27	1.0	27	21	AAA14004		Human liver glycogen
2	21	0.7	21	21	AAA14002		Human liver glycogen
c 3	21	0.7	21	21	AAA14003		Human liver glycogen
c 4	21	0.7	21	22	AAH62165		Phosphorylases glyc
5	21	0.7	21	22	AAH62166		Phosphorylases glyc
6	21	0.7	21	22	AAH62167		Phosphorylases glyc
7	21	0.7	21	22	AAH62168		Phosphorylases glyc
8	21	0.7	21	22	AAH62169		Phosphorylases glyc
9	21	0.7	21	22	AAH62170		Phosphorylases glyc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.

XX PR 19-JUL-1999; 99US-0357071.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Cowser LM;  
 XX DR WPI; 2000-270346/23.  
 XX PT Antisense compounds particularly oligonucleotides useful for prophylaxis, diagnosis and treatment of diseases associated with expression of liver glycogen phosphorylase  
 PT PT Example 13: Column 38; 33pp; English.  
 PS XX This sequence represents a human liver glycogen phosphorylase probe used in quantitative real-time PCR with primers AAA14002-A14003 in an exemplification of the present invention. The invention relates to antisense oligonucleotides targeted to the human liver glycogen phosphorylase gene (PYGL gene) which inhibit its expression. A series of oligonucleotides (AAA14008-A1404) were designed to target different regions of human liver glycogen phosphorylase RNA, and were analysed for their effect on liver glycogen phosphorylase levels by quantitative real-time PCR. GAPDH (glyceraldehyde-3'-phosphate) mRNA levels were measured as a control. Liver glycogen phosphorylase is one of three glycogen phosphorylase isozymes, which differ in their tissue-specific distribution, immunological properties and electrophoretic mobilities and are encoded by three different genes. Liver glycogen phosphorylase is encoded by the PYGL gene, which is located on chromosome 14. Liver glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase, and HGPa in its phosphorylated, active form) catalyses the degradation of stored glycogen in the liver to glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds. It therefore plays a critical role in carbohydrate metabolism and blood glucose homeostasis. Inhibition of liver glycogen phosphorylase and therefore glycogenolysis may provide a means of reducing blood glucose levels in diabetic patients, particularly those with type II (non insulin-dependent) diabetes. The antisense oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with liver glycogen phosphorylase expression, or those which may benefit from inhibition of liver glycogen phosphorylase expression, such as type II diabetes.  
 Sequence 27 BP; 5 A; 6 C; 8 G; 8 T; 0 other;  
 SQ Query Match 1.0%; Score 27; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 YY 437 ctgtatggccattacaaatcttgcgttgg 463  
 Db 1 ctgtatggccattacaaatcttgcgttgg 27  
 RESULT 2  
 AAA14002 ID AAA14002 standard; DNA: 21 BP.  
 XX AC  
 XX DT 18-JUL-2000 (first entry)  
 DE Human liver glycogen phosphorylase quantitative real-time PCR primer #2.  
 XX Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;  
 KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;  
 KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;  
 KW expression inhibition; antisense therapy; hypoglycaemic;  
 KW type II diabetes; non insulin-dependent;  
 KW quantitative real-time PCR primer; ss.  
 XX Homo sapiens.

XX PN US6043091-A.  
 XX PD 28-MAR-2000.  
 XX PF 19-JUL-1999; 99US-0357071.  
 XX PR 19-JUL-1999; 99US-0357071.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Cowser LM;  
 XX DR WPI; 2000-270346/23.  
 XX PT Antisense compounds particularly oligonucleotides useful for prophylaxis, diagnosis and treatment of diseases associated with expression of liver glycogen phosphorylase  
 PS XX Example 13: Column 38; 33pp; English.  
 XX Sequences AAA14002-A14003 represent human liver glycogen phosphorylase PCR primers used in quantitative real-time PCR with probe AAA14003 in an exemplification of the present invention. The invention relates to antisense oligonucleotides targeted to the human liver glycogen phosphorylase gene (PYGL gene), which inhibit its expression. A series of oligonucleotides (AAA14008-A14047) were designed to target different regions of human liver glycogen phosphorylase RNA, and were analysed for their effect on liver glycogen phosphorylase levels by quantitative real-time PCR. GAPDH (glyceraldehyde-3'-phosphate) mRNA levels were measured as a control. Liver glycogen phosphorylase is one of three glycogen phosphorylase isozymes, which differ in their tissue-specific distribution, immunological properties and electrophoretic mobilities and are encoded by three different genes. Liver glycogen phosphorylase is encoded by the PYGL gene, which is located on chromosome 14. Liver glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase, and HGPa in its phosphorylated, active form) catalyses the degradation of stored glycogen in the liver to glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds. It therefore plays a critical role in carbohydrate metabolism and blood glucose homeostasis. Inhibition of liver glycogen phosphorylase and therefore glycogenolysis may provide a means of reducing blood glucose levels in diabetic patients, particularly those with type II (non insulin-dependent) diabetes. The antisense oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with liver glycogen phosphorylase expression, or those which may benefit from inhibition of liver glycogen phosphorylase expression, such as type II diabetes.  
 CC Query Match 0.7%; Score 21; DB 21; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+04;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 other;  
 YY 386 catggccgaaattacaaatcaaaggaa 406  
 Db 1 catggccgaaattacaaatcaaaggaa 21  
 RESULT 3  
 AAA1403/C  
 ID AAA14003 standard; DNA: 21 BP.  
 XX AC AAA14003  
 XX DT 18-JUL-2000 (first entry)  
 DE Human liver glycogen phosphorylase quantitative real-time PCR primer #3.  
 XX Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;  
 KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;

KW glycoxygenolysis; carbohydrate metabolism; blood glucose homeostasis;  
 KW expression inhibition; antisense therapy; hypoglycaemic;  
 KW type II diabetes; non insulin-dependent;  
 KW quantitative real-time PCR primer; ss.  
 XX Homo sapiens.  
 OS US6043091-A.  
 XX PN XX  
 XX PD 28-MAR-2000.  
 XX FF 19-JUL-1999; 99US-0357071.  
 XX PR 19-JUL-1999; 99US-0357071.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Cowpert LM;  
 XX DR WPI; 2000-270346/23.  
 XX PS Example 13; Column 38; 33pp; English.  
 CC Sequences AAA14002-A14003 represent human liver glycogen phosphorylase  
 CC PCR primers used in quantitative real-time PCR with probe AAA14003 in an  
 CC exemplification of the present invention. The invention relates to  
 CC antisense oligonucleotides targetted to the human liver glycogen  
 CC phosphorylase gene (PYGL gene), which inhibit its expression. A series  
 CC of oligonucleotides (AAA14008-A14047) were designed to target different  
 CC regions of human liver glycogen phosphorylase RNA, and were analysed for  
 CC their effect on liver glycogen phosphorylase levels by quantitative  
 CC real-time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were  
 CC measured as a control. Liver glycogen phosphorylase is one of three  
 CC glycogen phosphorylase isozymes, which differ in their tissue-specific  
 CC distribution, immunological properties and electrophoretic mobilities  
 CC and are encoded by three different genes. Liver glycogen phosphorylase  
 CC is encoded by the PYGL gene, which is located on chromosome 14. Liver  
 CC glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate  
 CC alpha-D-glucosyltransferase, and HGuaP in its phosphorylated, active  
 CC form) catalyses the degradation of stored glycogen in the liver to  
 CC glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds.  
 CC It therefore plays a critical role in carbohydrate metabolism and blood  
 CC glucose homeostasis. Inhibition of liver glycogen phosphorylase and  
 CC therefore glycogenolysis may provide a means of reducing blood glucose  
 CC levels in diabetic patients, particularly those with type II (non  
 CC insulin-dependent) diabetes. The antisense oligonucleotides  
 CC of the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with liver glycogen phosphorylase expression, or  
 CC those which may benefit from inhibition of liver glycogen phosphorylase  
 CC expression, such as type II diabetes.  
 XX Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 other;

Query Match 0.78; Score 21; DB 21; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+04;  
 Matches 21; Conservative 0; Indels 0; Gaps 0;  
 Qy 505 gacttggcaatgggtgtcttg 525  
 Db 21 GACTTGGCAATGGGTGTCTTG 1

RESULT 4  
 AAH62165

ID AAH62165 standard; DNA; 21 BP.  
 XX AC AAH62165;  
 AC AAH62165;

DT 12-SEP-2001 (first entry)  
 XX Phosphorylaes glycogen polymorphism containing DNA fragment #6.  
 DE XX  
 KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;  
 KW heart disease; paternity testing; forensic science; ds.  
 KW XX  
 OS Homo sapiens.  
 XX XX  
 Key FH Location/Qualifiers  
 Variation FT replace(11,G)  
 /\*tag\*/ a /standard\_name= "single nucleotide polymorphism"  
 XX XX  
 PN WO200138576-A2.  
 XX XX  
 PD 31-MAY-2001.  
 XX XX  
 PF 17-NOV-2000; 2000WO-US31639.  
 PT XX  
 PR 24-NOV-1999; 99US-0167334.  
 XX XX  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 PT PA  
 PT XX  
 PI Cargill M, Ireland JS, Lander ES;  
 XX XX  
 DR WPI; 2001-367705/38.  
 XX XX  
 PT New nucleic acid segments of the human genome, particularly from genes which  
 PT including polymorphic sites, for phenotype correlation, forensics,  
 PT Paternity testing, medicine and genetic analysis -  
 XX XX  
 PS Claim 1; Page 34; 80pp; English.  
 CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
 CC contain single nucleotide polymorphisms (SNPs). A method is included in  
 CC the invention for analysing a nucleic acid sample, which consists of  
 CC determining the base occupying any one of the polymorphic sites given in  
 CC the SNP containing sequences. The nucleotide sequences can be used in the  
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
 CC diseases, diseases of the cardiovascular system, and infection by  
 CC microorganisms. The oligonucleotides are also useful in the manufacture  
 CC of a pharmaceutical. SNP containing oligonucleotides are useful in  
 CC applications such as phenotype correlation, forensics, paternity testing,  
 CC medicine and genetic analysis.  
 XX SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 other;  
 XX SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 other;  
 XX SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 other;

Query Match 0.78; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+04;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1218 aaccagaagacccgtccctac 1238  
 Db 1 aaccaaagacccgtccctac 21

RESULT 5  
 AAH62166

ID AAH62166 standard; DNA; 21 BP.  
 XX AC AAH62166;  
 AC AAH62166;

XX DT 12-SEP-2001 (first entry)  
 XX Phosphorylaes glycogen polymorphism containing DNA fragment #67.  
 KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;  
 KW heart disease; paternity testing; forensic science; ds.  
 KW XX  
 OS Homo sapiens.

Key	Location/Qualifiers
FH	replace(11,A)
FT	/tag= a
FT	/standard_name= "single nucleotide polymorphism"
XX	
PN	WO200138576-A2 .
XX	
31-MAY-2001 .	
XX	(WHED ) WHITEHEAD INST BIOMEDICAL RES .
PD	31-MAY-2001 .
PF	17-NOV-2000; 2000WO-US31639 .
XX	
PR	24-NOV-1999; 99US-0167334 .
XX	
PA	(WHED ) WHITEHEAD INST BIOMEDICAL RES .
XX	
PI	Cargill M, Ireland JS, Lander ES;
XX	
DR	WPI; 2001-367/05/38 .
XX	
PR	New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis -
PT	
PT	
PT	
XX	
PS	Claim 1; Page 34; 80pp; English.
XX	
DR	DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis .
XX	
CC	DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis .
XX	
PS	Claim 1; Page 34; 80pp; English.
XX	
CC	DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis .
XX	
PS	Sequence 21 BP; 4 A; 8 C; 6 G; 3 T; 0 other;
XX	
SQ	Query Match Score 21; DB 22; Length 21; Best Local Similarity 100.0%; Pred. No. 4.6e-04; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;
XX	
RESULT	7
Qy	AAH62168
ID	AAH62168 standard; DNA; 21 BP .
XX	
AC	AAH62168;
XX	
DE	12-SEP-2001 (first entry)
XX	
XX	Phosphorylaes glycogen polymorphism containing DNA fragment #69 .
XX	
XX	Single nucleotide polymorphism; SNP; human; cancer; inflammation; heart disease; paternity testing; forensic science; ds.
XX	
OS	Homo sapiens .
XX	
OS	WO200138576-A2 .
XX	
PD	31-MAY-2001 .
XX	
FH	Location/Qualifiers
FT	replace(11,A)
FT	/tag= a
FT	/standard_name= "single nucleotide polymorphism"
XX	
PN	WO200138576-A2 .
XX	
Key	Location/Qualifiers
Variation	replace(11,A)
FT	/tag= a
FT	/standard_name= "single nucleotide polymorphism"
XX	
PR	24-NOV-1999; 99US-0167334 .
XX	
PA	(WHED ) WHITEHEAD INST BIOMEDICAL RES .
XX	



CC diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis.

XX Sequence 21 BP; 8 A; 3 C; 9 G; 1 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.6e+04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2279 ggacagaaaggtaaggcc 2299

Db 1 ggacagaaaggtaaggcc 21

RESULT 10

ID AAH62171 standard; DNA; 21 BP.

XX AAH62171;

XX 12-SEP-2001 (first entry)

XX Phosphorylases glycogen polymorphism containing DNA fragment #72.

XX Single nucleotide polymorphism; SNP human; cancer; inflammation;

XX heart disease; paternity testing; forensic science; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT replace(11,T)

FT /\*tag= a

FT /standard\_name= "single nucleotide polymorphism"

XX PN WO2001138576-A2.

XX 31-MAY-2001.

XX PD 17-NOV-2000; 2000WO-US31639.

XX PR 24-NOV-1999; 99US-0167334.

XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX PI Cargill M, Ireland JS, Lander ES;

XX DR WPI; 2001-367705/38.

XX New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis

XX PS Claim 1; Page 35; 80pp; English.

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given in the SNP containing sequences. The nucleic acid sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonucleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in applications such as phenotype correlation, forensics, paternity testing, medicine and genetic analysis.

XX Sequence 21 BP; 3 A; 4 C; 3 G; 11 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.6e+04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2350 ttgacaatgttttttttttc 2370

Db 1 ttgacaatggcttttttttc 21

RESULT 11

ID AAF97015 standard; DNA; 21 BP.

XX AAF97015;

XX AC

XX DT 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #1776.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

XX polymorphism; vascular disease; coronary artery disease; forensics;

XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

XX pulmonary embolism; paternity test; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT replace(11,C)

FT /\*tag= a

FT /standard\_name= "single nucleotide polymorphism"

XX PN WO200118250-A2.

XX PR 15-MAR-2001.

XX PF 07-SEP-2000; 2000WO-US24503.

XX XX 10-SEP-1999; 99US-0153357.

XX PR 26-JUL-2000; 2000US-0220947.

XX PR 16-AUG-2000; 2000US-0225724.

XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX DR WPI; 2001-226749/23.

XX PA Nucleic acids comprising single nucleotide polymorphisms, useful in

PT PT analysis such as forensics, paternity testing, medicine, genetic

PT PT analysis and phenotype correlations to diseases such as diabetes and

PT atherosclerosis -

XX Examples: Page 166; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease

CC CC in an individual, involving determining the sequence at various

CC CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4

CC CC genes. The sequences at a number of polymorphic sites are also provided

CC CC in the specification. In particular, the method can be used in the

CC CC diagnosis of atherosclerosis, myocardial infarction, coronary heart

CC CC disease, stroke, peripheral vascular diseases, venous thromboembolism

CC CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

CC CC useful in forensics, paternity testing, genetic analysis and phenotype

CC CC correlations to diseases. The present sequence is an example of one of

CC CC the human gene SNPs shown in the specification.

XX Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 other;

XX Query Match 0.7%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 4 .6e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1123 agctgaatgtactaccc 1143  
 ||||| ||||| |||||  
 Db 1 agctgaatgtactaccc 21  
 ||||| |||||

RESULT 12

AAF97016 AAF97016 standard; DNA; 21 BP.

XX ID AAF97016;  
 AC AAF97016;  
 XX DT 06-JUN-2001 (first entry)

DE Human gene single nucleotide polymorphism #1778.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.

XX KW Homo sapiens.

OS Homo sapiens.

FH Key Variation Location/Qualifiers replace(11,C)  
 FT FT /\*tag= a /standard\_name= "single nucleotide polymorphism"  
 FT FT /\*tag= a /standard\_name= "single nucleotide polymorphism"  
 PN WO200118250-A2.

XX PD 15-MAR-2001.  
 XX PR 07-SEP-2000; 2000WO-US24503.  
 XX PR 10-SEP-1999; 99US-0153357.  
 XX PR 26-JUL-2000; 2000US-0220947.  
 XX PR 16-AUG-2000; 2000US-0225724.  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
 XX DR WPI; 2001-226749/23.  
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis -  
 PT Examples; Page 166; 242pp; English.  
 PS Examples; Page 166; 242pp; English.

CC The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPs shown in the specification.

SQ Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 other;

Query Match 0.7%; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4 .6e+04;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1873 tgtacaaccgcaattaaagaag 1893  
 ||||| |||||  
 Db 1 tgtacaaccgcaattaaagaag 21

XX Query Match 0.7%; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4 .6e+04;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 ID AAF97018  
 ID AAF97018 standard; DNA; 21 BP.  
 XX  
 AC AAF97018;  
 XX  
 DT 06-JUN-2001 (first entry)  
 DE Human gene single nucleotide polymorphism #1779.  
 XX  
 DE Human variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW Polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.  
 XX  
 Homo sapiens.  
 OS Homo sapiens.  
 PH Key Variation  
 PT Location/Qualifiers  
 FT replace(11,G)  
 FT /standard\_name= "single nucleotide polymorphism"  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX WO200118250-A2.  
 PN WO200118250-A2.  
 PD 15-MAR-2001.  
 XX  
 PR 07-SEP-2000; 2000WO-US24503.  
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 PR 10-SEP-1999; 99US-0153357.  
 PR 26-JUL-2000; 2000US-0220947.  
 PR 16-AUG-2000; 2000US-0225724.  
 XX  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
 DR WPI: 2001-226749/23.  
 XX  
 PR Nucleic acids comprising single nucleotide polymorphisms, useful in  
 PT applications such as forensics, paternity testing, medicine, genetic  
 PT analysis and phenotype correlations to diseases such as diabetes and  
 PT atherosclerosis -  
 XX  
 PS Examples: Page 166: 242pp; English.  
 XX  
 CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification.  
 XX Sequence 21 BP; 8 A; 3 C; 4 G; 6 T; 0 other;  
 XX  
 Query Match 0.7%; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+04;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1377 gatgtggaccctctgagaagg 1397  
 Db 1 gatgtggaccctctgagaagg 21  
 YY 2027 aagcaagtgtgaaagtcatctt 2047  
 Db 1 aagcaagtgtgaaagtcatctt 21  
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 Job time: 6483 sec  
 RESULT 15



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## OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 23:49:24 ; Search time 65.96 Seconds  
(without alignments)  
10531.406 Million cell updates/sec

Title: US-10-019-470-1  
Perfect score: 2828

Sequence: 1 gtttgaaggctctggcgagg. .... aaagtgtcaatttccaaggaa 2828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters:

403436

Minimum DB seq length: 0  
Maximum DB seq.length: 30  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /con2\_6/poddata/2/ina/6A\_COMB.seq;\*  
4: /con2\_6/poddata/2/ina/6B\_COMB.seq;\*  
5: /con2\_6/poddata/2/ina/pcmts.COMB.seq;\*  
6: /cgn2\_6/poddata/2/ina/backfiles1.seq;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	1.0	27	3 US-09-357-071-4	Sequence 4, Appli
2	21	0.7	21	3 US-09-357-071-2	Sequence 2, Appli
c 3	21	0.7	21	3 US-09-357-071-3	Sequence 3, Appli
c 4	20	0.7	20	3 US-09-357-071-8	Sequence 8, Appli
c 5	20	0.7	20	3 US-09-357-071-9	Sequence 9, Appli
c 6	20	0.7	20	3 US-09-357-071-10	Sequence 10, Appli
c 7	20	0.7	20	3 US-09-357-071-11	Sequence 11, Appli
c 8	20	0.7	20	3 US-09-357-071-12	Sequence 12, Appli
c 9	20	0.7	20	3 US-09-357-071-13	Sequence 13, Appli
c 10	20	0.7	20	3 US-09-357-071-14	Sequence 14, Appli
c 11	20	0.7	20	3 US-09-357-071-15	Sequence 15, Appli
c 12	20	0.7	20	3 US-09-357-071-16	Sequence 16, Appli
c 13	20	0.7	20	3 US-09-357-071-17	Sequence 17, Appli
c 14	20	0.7	20	3 US-09-357-071-18	Sequence 18, Appli
c 15	20	0.7	20	3 US-09-357-071-19	Sequence 19, Appli
c 16	20	0.7	20	3 US-09-357-071-20	Sequence 20, Appli
c 17	20	0.7	20	3 US-09-357-071-21	Sequence 21, Appli
c 18	20	0.7	20	3 US-09-357-071-22	Sequence 22, Appli
c 19	20	0.7	20	3 US-09-357-071-23	Sequence 23, Appli
c 20	20	0.7	20	3 US-09-357-071-24	Sequence 24, Appli
c 21	20	0.7	20	3 US-09-357-071-25	Sequence 25, Appli
c 22	20	0.7	20	3 US-09-357-071-26	Sequence 26, Appli
c 23	20	0.7	20	3 US-09-357-071-27	Sequence 27, Appli
c 24	20	0.7	20	3 US-09-357-071-28	Sequence 28, Appli
c 25	20	0.7	20	3 US-09-357-071-29	Sequence 29, Appli
c 26	20	0.7	20	3 US-09-357-071-30	Sequence 30, Appli
c 27	20	0.7	20	3 US-09-357-071-31	Sequence 31, Appli

RESULTS 1  
US-09-357-071-4  
; Sequence 4, Application US/09357071  
; Patent No. 6043091  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSTO  
; FILE REFERENCE: RTS-0074  
; CURRENT APPLICATION NUMBER: US/09/357,071  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 4  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Probe  
US-09-357-071-4

ALIGNMENTS

Query Match Best Local Similarity 1.0%; Score 27; DB 3; Length 27;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-357-071-2  
; Sequence 2, Application US/09357071  
; Patent No. 6043091  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSTO  
; FILE REFERENCE: RTS-0074  
; CURRENT APPLICATION NUMBER: US/09/357,071  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 2  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Probe  
US-09-357-071-2

Query Match 0.7%; Score 21; DB 3; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 catggccgaattacaga 406  
 Db 1 catggccgaattacaga 21

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 ; Sequence 3, Application US/09357071  
 ; Patent No. 6043091  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
 ; FILE REFERENCE: RTS-0074  
 ; CURRENT APPLICATION NUMBER: US/09/357,071  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 3  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: PCR Primer  
 US-09-357-071-3

Query Match 0.7%; Score 21; DB 3; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 gacttggcaatggtgtcttg 525  
 Db 21 GACTTGGCAATGGTGTCTTG 1

RESULT 4  
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 ; Patent No. 6043091  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
 ; FILE REFERENCE: RTS-0074  
 ; CURRENT APPLICATION NUMBER: US/09/357,071  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 8  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-357-071-8

Query Match 0.7%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ctctcgccgcggggggcgg 28  
 Db 20 ctctcgccgcggggggcgg 1

RESULT 5  
 \*US-09-357-071-9/C  
 ; Sequence 9, Application US/09357071

Query Match 0.7%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 ccagcttcgtcgagccgg 90  
 Db 20 CCAGCTTCGTGCGAGCCCG 1

RESULT 6  
 \*US-09-357-071-10/C  
 ; Sequence 10, Application US/09357071  
 ; Patent No. 6043091  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
 ; FILE REFERENCE: RTS-0074  
 ; CURRENT APPLICATION NUMBER: US/09/357,071  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 10  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-357-071-10

Query Match 0.7%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 cagccatggcgaacctgtg 128  
 Db 20 CAGCCATGGCGAACCGCTG 1

RESULT 7  
 \*US-09-357-071-11/C  
 ; Sequence 11, Application US/09357071  
 ; Patent No. 6043091  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
 ; FILE REFERENCE: RTS-0074  
 ; CURRENT APPLICATION NUMBER: US/09/357,071  
 ; CURRENT FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 11  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
RESULT 8 US-09-357-071-12/c
Query Match Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 114 atgggaaacctgtacaga 133
Db 20 ATGGGAAACCGCTGACAGA 1

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTIS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-12

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
RESULT 9 US-09-357-071-13/c
Query Match Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 172 tggctggaaacctggca 191
Db 20 TGGCCTGGAAACCTGGCA 1

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTIS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-13

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
RESULT 10 US-09-357-071-14/c
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 114 atgggaaacctgtacaga 133
Db 20 ATGGGAAACCGCTGACAGA 1

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTIS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-14

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTIS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-15

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTIS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-16

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTIS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-17

; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTIS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-18

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; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-16

RESULT 15
Qy 460 ttggattttatggatataaaagg 479
Db 20 TTGGATTGGATATGAGAG 1

US-09-357-071-19/C
; Sequence 19, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; ATTORNEY: Lex M. Cowseit
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-19

Query Match 0.7%
Best Local Similarity 100.0%
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SEQ ID NO 372 ttcctggaaatttacatggg 391
Db 20 TCTCTGAAATTTACATGGG 1

RESULT 13
US-09-357-071-17/C
; Sequence 17, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; ATTORNEY: Lex M. Cowseit
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-17

Query Match 0.7%
Best Local Similarity 100.0%
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SEQ ID NO 523 ttggggacttgcgtgc 542
Db 20 TTGGGAGACTGCTGTGTC 1

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Job time: 8125 sec

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Query Match 0.7%
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SEQ ID NO 415 tcaacctcggtgtcggaaaat 434
Db 20 TCACCCCGGGTGTGCAAAAT 1

RESULT 14
US-09-357-071-18/C
; Sequence 18, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; ATTORNEY: Lex M. Cowseit
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-18

Query Match 0.7%
Best Local Similarity 100.0%
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## OM nucleic - nucleic search, using sw model

Run on : September 7, 2002, 00:29:44 ; Search time 3515.76 Seconds

(without alignments)  
 17402.637 Million cell updates/secTitle: US-10-019-470-1  
 Perfect score: 2828

Sequence: 1 gttaaaaagcttctggcg...aaatgttccaaaggaa 2828

## Scoring table:

IDENTITY NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
 Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	27	1.0	37	US-10-019-470-4		Sequence 4 , Appli
3	21	0.7	21	PCP-US00-19019-2		Sequence 2 , Appli
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c	5	21	0.7	21	1	PCP-US00-19019-2
c	6	21	0.7	21	37	Sequence 2 , Appli
c	7	20.6	0.7	21	25	Sequence 3 , Appli
c	8	20.6	0.7	21	25	Sequence 1780 , AP
c	9	20.6	0.7	21	25	Sequence 1782 , AP
c	10	20.6	0.7	21	25	Sequence 1783 , AP
c	11	20.6	0.7	21	25	Sequence 1784 , AP
c	12	20.6	0.7	21	28	Sequence 66 , AP
c	13	20.6	0.7	21	28	Sequence 72 , AP
c	14	20.6	0.7	21	35	Sequence 449800 , AP
c	15	20.6	0.7	21	35	Sequence 552400 , AP
c	16	20.6	0.7	21	28	Sequence 437570 , AP
c	17	20.6	0.7	21	28	Sequence 51131 , AP
c	18	20.6	0.7	21	28	Sequence 8 , Appli
c	19	20.2	0.7	20	1	Sequence 9 , Appli
c	20	20.2	0.7	20	1	Sequence 10 , Appli
c	21	20.2	0.7	20	1	Sequence 11 , Appli
c	22	20.2	0.7	20	1	Sequence 13 , Appli
c	23	20	0.7	20	1	Sequence 14 , Appli
c	24	20	0.7	20	1	Sequence 15 , Appli
c	25	20	0.7	20	1	Sequence 16 , Appli

RESULT **1**  
PCT-US00-19019-4  
; Sequence 4, Application PC/TUS0019019  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowser  
; APPLICANT: ISIS PHARMACEUTICALS, Inc.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
; FILE REFERENCE: RTSP-0056  
; CURRENT APPLICATION NUMBER: PCT/US00/19019  
; CURRENT FILING DATE: 2000-07-12  
; EARLIER APPLICATION NUMBER: US 09/357,071  
; EARLIER FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 4  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Probe  
PCT-US00-19019-4

## ALIGNMENTS

Query Match 1.0%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 4.2e+04;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Sequence 17, Appl  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 20, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 23, Appl  
Sequence 24, Appl  
Sequence 25, Appl  
Sequence 26, Appl  
Sequence 27, Appl  
Sequence 28, Appl  
Sequence 29, Appl  
Sequence 30, Appl  
RESULT **3**  
PCT-US00-19019-2  
; Sequence 2, Application PC/TUS0019019  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowser  
; APPLICANT: ISIS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
; FILE REFERENCE: RTSP-0056  
; CURRENT APPLICATION NUMBER: PCT/US00/19019  
; CURRENT FILING DATE: 2000-07-12  
; EARLIER FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 2  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
PCT-US00-19019-2

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Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 catggccgacattacagaa 21

RESULT **4**  
PCT-US00-19019-3/c  
; Sequence 3, Application PC/TUS0019019  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowser  
; APPLICANT: ISIS PHARMACEUTICALS, Inc.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
; FILE REFERENCE: RTSP-0056  
; CURRENT APPLICATION NUMBER: PCT/US00/19019  
; CURRENT FILING DATE: 2000-07-12  
; EARLIER APPLICATION NUMBER: US 09/357,071  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 3  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
PCT-US00-19019-3

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Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
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Db 21 GACTTGGCAATGGGGCTTG 1

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; Sequence 4, Application US/10019470  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowser  
; APPLICANT: ISIS PHARMACEUTICALS, Inc.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
; FILE REFERENCE: RTSP-0240  
; CURRENT APPLICATION NUMBER: US/10/019,470  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357,071  
; PRIOR FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 4  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Probe  
US-10-019-470-4

RESULT 5  
US-10-019-470-2  
; Sequence 2, Application US/10019470  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
; FILE REFERENCE: RNSP-0240  
; CURRENT APPLICATION NUMBER: US/10/019,470  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357,071  
; PRIOR FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 2  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-019-470-2

Query Match 0.7%; Score 21; DB 37; Length 21;  
Best Local Similarity 100%; Pred. No. 1.1e+06;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 catggccgaaattacagaa 406  
Db 1 catggccgaaattacagaa 21

RESULT 6  
US-10-019-470-3/c  
; Sequence 3, Application US/10019470  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION  
; FILE REFERENCE: RNSP-0240  
; CURRENT APPLICATION NUMBER: US/10/019,470  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357,071  
; PRIOR FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 3  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-019-470-3

Query Match 0.7%; Score 21; DB 37; Length 21;  
Best Local Similarity 100%; Pred. No. 1.1e+06;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 gacttgcataatgggtgtctc 525  
Db 21 GACTTGCATAATGGGTGTC 1

RESULT 7  
US-09-657-472-1780  
; Sequence 1780, Application US/09657472  
; GENERAL INFORMATION:  
; APPLICANT: Lander, Eric S.  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Bolk, Stacey  
; APPLICANT: McCarthy, Jeanette J.  
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES  
; FILE REFERENCE: 2825.1027-001  
; CURRENT APPLICATION NUMBER: US/09/657,472  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: US 60/153,357  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 60/220,947  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: US 60/225,724  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2551  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1780  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-657-472-1781

Query Match 0.7%; Score 20.6; DB 25; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.4e+06;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1123 agctgtatgtatcttcctc 1143  
Db 1 agctgtatgtatcttcctc 21

RESULT 8  
US-09-657-472-1781  
; Sequence 1781, Application US/09657472  
; GENERAL INFORMATION:  
; APPLICANT: Lander, Eric S.  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Bolk, Stacey  
; APPLICANT: McCarthy, Jeanette J.  
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES  
; FILE REFERENCE: 2825.1027-001  
; CURRENT APPLICATION NUMBER: US/09/657,472  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: US 60/153,357  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 60/220,947  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: US 60/225,724  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2551  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1781  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-657-472-1781

Query Match 0.7%; Score 20.6; DB 25; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.4e+06;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1978 agctgtatgtatcttcgtggcag 1998  
Db 1 agctgtatgtatcttcgtggcag 21

RESULT 9  
US-09-657-472-1782  
; Sequence 1782, Application US/09657472  
; GENERAL INFORMATION:  
; APPLICANT: Lander, Eric S.  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Bolk, Stacey  
; APPLICANT: McCarthy, Jeanette J.  
; APPLICANT: Ireland, James S.  
; APPLICANT: Bolk, Stacey

Query Match 0.7%; Score 20.6; DB 25; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.4e+06;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.107-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1782
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; SEQ-ID-NOS: US-09-657-472-1782

Query Match          0.7%;  Score 20.6;  DB 25;  Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1873 tgcataaccgtatagaag 1893
Db      1 tgacaaaccgtatagaag 21

RESULT 10
US-09-657-472-1783
Sequence 1783, Application US/09657472
GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIORITY APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIORITY APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIORITY APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1784
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; SEQ-ID-NOS: US-09-657-472-1784

Query Match          0.7%;  Score 20.6;  DB 25;  Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1377 gatgtggaccctctgagaagg 1397
Db      1 gatgtggaccctctgagaagg 21

RESULT 12
US-09-715-849-66
Sequence 66, Application US/09715849
GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2002-001
; CURRENT APPLICATION NUMBER: US/09/715,849
; CURRENT FILING DATE: 2000-11-17
; PRIORITY APPLICATION NUMBER: US 60/167,334
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 66
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; SEQ-ID-NOS: US-09-715-849-66

Query Match          0.7%;  Score 20.6;  DB 28;  Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1218 acccagaagaccttcgcctac 1238
Db      1 aaccagaagaccttcgcctac 21

RESULT 13
US-09-715-849-67
Sequence 67, Application US/09715849
GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2002-001

Query Match          0.7%;  Score 20.6;  DB 25;  Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      2027 aaccaaggtaaagtcattt 2047
Db      1 aaccaaggtaaagtcattt 21

RESULT 14
US-09-657-472-1783
Sequence 1783, Application US/09657472
GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.

```

```

; CURRENT APPLICATION NUMBER: US/09/715,849
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/167,334
; PRIORITY FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 67
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-715-849-67

```

```

RESULT 14
US-09-715-849-68
; Sequence 68, Application US/09715849
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele S.
; APPLICANT: Ireland, James S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825_2002-001
; CURRENT APPLICATION NUMBER: US/09/715,849
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/167,334
; PRIORITY FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 68
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-715-849-68

```

```

RESULT 14
US-09-715-849-68
; Sequence 68, Application US/09715849
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele S.
; APPLICANT: Ireland, James S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825_2002-001
; CURRENT APPLICATION NUMBER: US/09/715,849
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/167,334
; PRIORITY FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 68
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-715-849-68

```

```

RESULT 15
US-09-715-849-69
; Sequence 69, Application US/09715849
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele S.
; APPLICANT: Ireland, James S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825_2002-001
; CURRENT APPLICATION NUMBER: US/09/715,849
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/167,334
; PRIORITY FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 69
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-715-849-69

```

Search completed: September 7, 2002, 03:09:15  
Job time: 9571 sec

```

Query Match          0.7%; Score 20.6; DB 28; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy   2119 ctgcaggcaccgaaagctcg 2139
      |||||||:|||||||:|||||||:||| Db
      1 ctgcaggcaccygaagctcg 21

```

```

Query Match          0.7%; Score 20.6; DB 28; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+06;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy   1706 cctccggaaactcgccaagt 1726
      |||||||:|||||||:||| Db
      1 cctccggaaamtccgccaagt 21

```



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 01:05:04 ; Search time 495.36 Seconds  
(without alignments)  
1736.191 Million cell updates/sec

Title: US-10-019-470-1  
Perfect score: 2888  
Sequence: 1 gtttggaaatctggcgccgg.....aaagtgtcaatttccaaggaa 2828

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2036664 seqs, 1522705716 residues

Total number of hits satisfying chosen parameters: 888728

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0<sup>8</sup>  
Maximum Match 100<sup>8</sup>  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New \*

1: /cgn2\_6/podata/2/pr/a/PCT\_NEW\_COMBO.seq; \*  
2: /cgn2\_6/podata/2/pr/a/US06\_NEW\_COMBO.seq; \*  
3: /cgn2\_6/podata/2/pr/a/US07\_NEW\_COMBO.seq; \*  
4: /cgn2\_6/podata/2/pr/a/US08\_NEW\_COMBO.seq; \*  
5: /cgn2\_6/podata/2/pr/a/US09\_NEW\_COMBO.seq; \*  
6: /cgn2\_6/podata/2/pr/a/US10\_NEW\_COMBO.seq; \*  
7: /cgn2\_6/podata/2/pr/a/US10\_NEW\_COMBO.seq; \*  
8: /cgn2\_6/podata/2/pr/a/US06\_NEW\_COMBO.seq; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	1.0	27	7 US-10-114-544-4	Sequence 4, Appli
2	21	0.7	21	7 US-10-114-544-2	Sequence 2, Appli
c 3	21	0.7	21	7 US-10-114-544-3	Sequence 3, Appli
c 4	20	0.7	20	7 US-10-114-544-8	Sequence 8, Appli
c 5	20	0.7	20	7 US-10-114-544-9	Sequence 9, Appli
c 6	20	0.7	20	7 US-10-114-544-10	Sequence 10, Appli
c 7	20	0.7	20	7 US-10-114-544-11	Sequence 11, Appli
c 8	20	0.7	20	7 US-10-114-544-12	Sequence 12, Appli
c 9	20	0.7	20	7 US-10-114-544-13	Sequence 13, Appli
c 10	20	0.7	20	7 US-10-114-544-14	Sequence 14, Appli
c 11	20	0.7	20	7 US-10-114-544-15	Sequence 15, Appli
c 12	20	0.7	20	7 US-10-114-544-16	Sequence 16, Appli
c 13	20	0.7	20	7 US-10-114-544-17	Sequence 17, Appli
c 14	20	0.7	20	7 US-10-114-544-18	Sequence 18, Appli
c 15	20	0.7	20	7 US-10-114-544-19	Sequence 19, Appli
c 16	20	0.7	20	7 US-10-114-544-20	Sequence 20, Appli
c 17	20	0.7	20	7 US-10-114-544-21	Sequence 21, Appli
c 18	20	0.7	20	7 US-10-114-544-22	Sequence 22, Appli
c 19	20	0.7	20	7 US-10-114-544-23	Sequence 23, Appli
c 20	20	0.7	20	7 US-10-114-544-24	Sequence 24, Appli
c 21	20	0.7	20	7 US-10-114-544-25	Sequence 25, Appli
c 22	20	0.7	20	7 US-10-114-544-26	Sequence 26, Appli
c 23	20	0.7	20	7 US-10-114-544-27	Sequence 27, Appli
c 24	20	0.7	20	7 US-10-114-544-28	Sequence 28, Appli
c 25	20	0.7	20	7 US-10-114-544-29	Sequence 29, Appli

## ALIGNMENTS

RESULT 1  
US-10-114-544-4  
; Sequence 4, Application US/10114544  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTSP-0240  
; CURRENT APPLICATION NUMBER: US/10/114,544  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 10/019,470  
; PRIOR FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357,071  
; PRIOR FILING DATE: 1998-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 4  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Probe  
US-10-114-544-4

Query Match 1.0%; Score 27; DB 7; Length 27;  
Best Local Similarity 100.0%; Pred. No. 5.8e-03;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY ctgtgtgaggcccatttaccacgttgttg 463  
Db 1 ctgtgtgaggccatttaccacgttgttg 27

RESULT 2  
US-10-114-544-2  
; Sequence 2, Application US/10114544  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTSP-0240  
; CURRENT APPLICATION NUMBER: US/10/114,544  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 10/019,470  
; PRIOR FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357,071

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-8

Query Match          0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-2

Query Match          0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-3

Query Match          0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-4

Query Match          0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+05; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-5

Query Match          0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-6

Query Match          0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-7

Query Match          0.7%; Score 21; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-8

Query Match          0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 9
; LENGTH: 20
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; PRIORITY FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIORITY FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO: 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-9

Query Match          0.7%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
; SEQ ID NO: 10
; LENGTH: 20
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; PRIORITY FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIORITY FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO: 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-10

```

Query Match 0.7%; Score 20; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 109 cagccatgggaacgctgt 128  
 Db 20 CAGCCATGGCGAACGGCTG 1

RESULT 7  
 US-10-114-544-11/C  
 ; Sequence 1.1, Application US/10114544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; FILE REFERENCE: RUSP-0240  
 ; CURRENT APPLICATION NUMBER: US/10/114, 544  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 10/019, 470  
 ; PRIOR FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: US 09/357, 071  
 ; PRIOR FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 11  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; SEQ ID NO 13

Query Match 0.7%; Score 20; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 114 atggcgaacgctgacaga 133  
 Db 20 ATGGCGAACGGCTGACAGA 1

RESULT 8  
 US-10-114-544-12/C  
 ; Sequence 1.2, Application US/10114544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; FILE REFERENCE: RUSP-0240  
 ; CURRENT APPLICATION NUMBER: US/10/114, 544  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 10/019, 470  
 ; PRIOR FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: US 09/357, 071  
 ; PRIOR FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 12  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; SEQ ID NO 14

Query Match 0.7%; Score 20; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 172 tggcgctggaaacgtggca 191  
 Db 20 TGGCGCTGGAAACGTGGCA 1

RESULT 9  
 US-10-114-544-13/C  
 ; Sequence 1.3, Application US/10114544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Lex M. Cowert  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
 ; FILE REFERENCE: RUSP-0240  
 ; CURRENT APPLICATION NUMBER: US/10/114, 544  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 10/019, 470  
 ; PRIOR FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: US 09/357, 071  
 ; PRIOR FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 13  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; SEQ ID NO 15

Query Match 0.7%; Score 20; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 220 tgcaactcacgctggtaag 239  
 Db 20 TGCAACTCAGCTGGTCAAG 1

RESULT 10  
 US-10-114-544-14/C  
 ; Sequence 1.4, Application US/10114544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Lex M. Cowert  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
 ; FILE REFERENCE: RUSP-0240  
 ; CURRENT APPLICATION NUMBER: US/10/114, 544  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 10/019, 470  
 ; PRIOR FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: US 09/357, 071  
 ; PRIOR FILING DATE: 1999-07-19  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 14  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; SEQ ID NO 16

Query Match 0.7%; Score 20; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 260 ccgcactactacttcgcgc 279  
 Db 20 CCGCACTACTTCGC 1

RESULT 11  
US-10-114-544-15/c  
; Sequence 15, Application US/10114544  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RNSP-0240  
; CURRENT APPLICATION NUMBER: US/10/114, 544  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 10/019, 470  
; PRIOR FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357, 071  
; SEQ ID NO: 17  
; LENGTH: 20  
; NUMBER OF SEQ ID NOS: 47  
; PRIOR FILING DATE: 1999-07-19  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-114-544-15

Query Match 0.7%; Score 20; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

---

RESULT 12  
US-10-114-544-16/c  
; Sequence 16, Application US/10114544  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RNSP-0240  
; CURRENT APPLICATION NUMBER: US/10/114, 544  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 10/019, 470  
; PRIOR FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357, 071  
; SEQ ID NO: 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-114-544-16

Query Match 0.7%; Score 20; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

---

RESULT 13  
US-10-114-544-17/c  
; Sequence 17, Application US/10114544  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia

; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 10/019,470  
; PRIOR FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/357,071  
; PRIOR FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-114-544-19

Query Match 0.7%; Score 20; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 523 ttgggagacttgctgc 542  
Db 20 TTGGGAGACTGCTGCTGC 1

Search completed: September 7, 2002, 03:17:51  
Job time: 7967 sec

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Result No.	Score	Query Match	Length	DB ID	Description
1	17.2	0.6	28	12 AZ782046	AZ782046 2M0021N19
c 2	17.2	0.6	29	12 AZ514403	AZ514403 1M0361K06
c 3	16.6	0.6	30	12 AZ990068	AZ990068 2M0027G07
c 4	16.4	0.6	29	12 AZ331559	AZ331559 1M0059J06
c 5	16	0.6	26	10 D11539	D11539 HUN0C12B04
c 6	16	0.6	27	12 TA12806P	AL463342 T. brucei
c 7	16	0.6	28	12 AZ760461	AZ760461 1M0554C13
c 8	16	0.6	29	12 AZ323093	AZ323093 1M0044A07
c 9	16	0.6	29	12 AZ658502	AZ658502 1M0535M12
c 10	16	0.6	30	12 AZ458346	AZ458346 1M0262P13
c 11	15.8	0.6	23	12 AZ433969	AZ433969 1M0220B07
c 12	15.8	0.6	27	10 D25863	D25863 HUNGS04241
c 13	15.8	0.6	28	9 AI826975	AI826975 wks5a12.x
c 14	15.8	0.6	28	12 AZ793395	AZ793395 2M0055N16
c 15	15.8	0.6	29	12 AZ477226	AZ477226 1M0294F02
c 16	15.8	0.6	30	10 T63438	T63438 Yc07e02.r1
c 17	15.8	0.6	30	12 AZ433900	AZ433900 1M0220F03

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.2	0.6	28	12 AZ782046	AZ782046 2M0021N19
c 2	16.6	0.6	30	12 AZ514403	AZ514403 1M0361K06
c 4	16.4	0.6	29	12 AZ990068	AZ990068 2M0027G07
c 5	16	0.6	26	10 D11539	D11539 HUN0C12B04
c 6	16	0.6	27	12 TA12806P	AL463342 T. brucei
c 7	16	0.6	28	12 AZ760461	AZ760461 1M0554C13
c 8	16	0.6	29	12 AZ323093	AZ323093 1M0044A07
c 9	16	0.6	29	12 AZ658502	AZ658502 1M0535M12
c 10	16	0.6	30	12 AZ458346	AZ458346 1M0262P13
c 11	15.8	0.6	23	12 AZ433969	AZ433969 1M0220B07
c 12	15.8	0.6	27	10 D25863	D25863 HUNGS04241
c 13	15.8	0.6	28	9 AI826975	AI826975 wks5a12.x
c 14	15.8	0.6	28	12 AZ793395	AZ793395 2M0055N16
c 15	15.8	0.6	29	12 AZ477226	AZ477226 1M0294F02
c 16	15.8	0.6	30	10 T63438	T63438 Yc07e02.r1
c 17	15.8	0.6	30	12 AZ433900	AZ433900 1M0220F03

AL481055 T. brucei  
AZ832213 2M0112C03  
AI815551 au49b06.Y  
AZ458545 1M0262B15  
AL451961 T. brucei  
AI808531 wf95el12.X  
C21101 HUNGS000262  
C21203 HUNGS000223  
AZ579502 1M0361D12  
AZ648296 1M0517B10P  
AZ475143 1M0293G22  
AA027602 mi12d08.R  
AI687937 tp99d01.X  
AZ466667 1M0277G06  
AU014027 AU014027  
AZ587944 1M039Q023  
AZ421244 1M0198K20  
AL472082 T. brucei  
AZ807245 2M0065M24  
AZ485096 1M0312K10  
AZ811944 2M0087M12  
AZ831709 2M0111Q006  
AL475157 T. brucei  
AL479558 T. brucei  
AZ784264 2M0026120  
AZ400095 1M0165P19  
AZ658557 1M0536104  
AZ973344 2M0247H06

ALIGNMENTS

EST:\*

1: em\_estba:\*

2: em\_estbum:\*

3: em\_estin:\*

4: em\_esimu:\*

5: em\_estov:\*

6: em\_estp1:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_gss:\*

13: em\_gss\_hum:\*

14: em\_gss\_inv:\*

15: em\_gss\_pn:\*

16: em\_gss\_vrt:\*

RESULT 1

AZ782046 LOCUS 2M0021N19R Mouse 10kb Plasmid UGCC1M library Mus musculus genomic DEFINITION clone UGGC2M0021N19 R, DNA sequence. ACCESSION AZ782046 VERSION GSS KEYWORDS SOURCE ORGANISM Mammalia; Eutheria; Rodentia; Sciuromorphathi; Murinae; Mus. REFERENCES 1 (bases 1 to 28)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Lonacare, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 100000 Std. Error: 0.00 Place: 0021 row: N column: 19 Seq. primer: CACACAGAAAAGCTPATGACC Class: plasmid ends High quality sequence stop: 28. Location/Qualifiers 1. 28 /organism="Mus musculus" /strain="C57BL/6J" /db\_xref="taxon:10090" /clone="UGGC2M0021N19" /clone\_lib="Mouse 10kb plasmid UGCC1M library"

/sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
*musculus* C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnare/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (g1147321419b1AF129072.1), a copy-number  
 inducible derivative of Plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT	ORIGIN	Query Match Score	Length	DB	Best Local Similarity	Match No.	Best Local Similarity	Score	Length	DB
7	a	0.68;	28;	12;	86.4%	7.8e+06	86.4%	17.2;	29;	12;
9	c	0.68;	28;	12;	86.4%	7.8e+06	86.4%	17.2;	29;	12;
4	g	0.68;	28;	12;	86.4%	7.8e+06	86.4%	17.2;	29;	12;
8	t	0.68;	28;	12;	86.4%	7.8e+06	86.4%	17.2;	29;	12;

BASE COUNT	ORIGIN	Query Match Score	Length	DB	Best Local Similarity	Match No.	Best Local Similarity	Score	Length	DB
5	a	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14
6	c	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14
4	g	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14
9	t	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14

RESULT 2  
 A2514403/c AZ990068 LOCUS AZ990068 30 bp DNA LINEAR GSS 27-APR-2001  
 DEFINITION 2M0273G07R Mouse 10kb plasmid UGGC2M library Mus musculus genomic  
 clone UGGC2M0273G07 R, DNA sequence.  
 ACCESSION AZ990068  
 VERSION AZ990068.1 GI:13861295  
 KEYWORDS GSS,  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .  
 1 (bases 1 to 29)  
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 AUTHORS Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingay,A., von Niederhausern,A.,  
 and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0273 row: K column: 06  
 Seq primer: CGTGTAAAAACGAGCCGAGT  
 Class: Plasmid ends  
 High quality sequence stop: 29.  
 FEATURES Location/Qualifiers  
 source 1. -29  
 \* /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGC1M0361K06"

BASE COUNT	ORIGIN	Query Match Score	Length	DB	Best Local Similarity	Match No.	Best Local Similarity	Score	Length	DB
5	a	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14
6	c	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14
4	g	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14
9	t	0.68;	29;	14	86.4%	7.9e+06	86.4%	17.2;	29;	14

/clone="UUGC2M0273G07"  
 /clone\_1lib="Mouse 10kb plasmid UUGC2M 1 library"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD2nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://wwwjax.org/resources/documents/dnare/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT ORIGIN	7 a	7 c	8 g	11 t	BASE COUNT ORIGIN
Query Match Best Local Similarity Matches 19;	Score 16.6; Pred. No. 1.1e+07;	Score 16.4; Pred. No. 1.2e+07;	Score 16.4; Pred. No. 1.2e+07;	Length 30;	Query Match Best Local Similarity Matches 20;
Conservative 0;	Mismatches 4;	Mismatches 6;	Mismatches 6;	Length 29;	Conservative 0;
	Indels 0;	Indels 0;	Indels 0;		Gaps 0;
	Gaps 0;				

Qy 241 accgeaaacgtggccaccacccgc 263  
 "Db 8 ACCGGAACTGGACAGGACCCAC 30

RESULT 4  
 AZ331559/c  
 LOCUS AZ331559 29 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1m0059LGDR Mouse 10kb plasmid UGC1M 1 library Mus musculus genomic clone UGC1M0059LGDR, R, DNA sequence.  
 ACCESSION AZ331559  
 VERSION .1  
 GSS: GI:10394372  
 SOURCE house mouse.

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0059 row: L column: 06  
 Seq primer: CACACGAAACAGCATTGACC  
 Class: plasmid ends  
 High quality sequence stop: 29.

FEATURES source  
 1 - 29  
 /organism="Mus musculus"  
 /strain="C57BL/6J"

RESULT 5  
 D11539 26 bp mRNA linear EST 21-JUL-1994  
 DEFINITION HUMOC12B04 Liver HepG2 cell line. Homo sapiens cDNA clone c12B04  
 3' mRNA sequence.  
 Qy 726 99aaaggtaaaaaaccaacaacccgg 751  
 "Db 27 GGAAATGATGACACCCACACAGG 2

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Okubo, K., Horii, N., Matoba, R., Niizuma, T., Kojima, Y. and Matsubara, K.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Okubo, K., Horii, N., Matoba, R., Niizuma, T., Kojima, Y.  
 TITLE Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression  
 JOURNAL Nature Genet. 2, 173-179 (1992)  
 MEDLINE 94238199  
 COMMENT Contact: Koussaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Niizuma, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 1-3 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES source  
 1 - 26  
 /organism="Homo sapiens"  
 /db\_xref="GDB:0058041E"  
 /db\_xref="taxon:9606"  
 /clone="c12B04"  
 /clone\_1lib="Liver HepG2 cell line."  
 /lab\_host="E.coli"  
 /note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."  
 12 a 2 c 5 g 7 t

Eukaryota	Metazoa	Chordata	Craniata	Vertebrata	Euteleostomi
Mammalia	Eutheria	Rodentia	Sciurognathi	Muridae	Mus
1 (bases 1 to 28)	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hanif,C., Reilly,Islam,H., Longacre,S., Mahmoud,M., Meenah,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.				
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	Mouse whole genome scaffolding with paired end reads from 10kb				
Db	2 ATCAAAGAAATTGATTAATGT 25				
RESULTS	6				
LOCUS	TAA128C06P/c	TAA128C06P	27 bp	DNA	linear GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 128c06, forward sequence, genomic survey sequence.				
ACCESSION	AL464342	GI:11834605			
VERSION	AL464342.1	GI:11834605			
KEYWORDS	GSS.				
SOURCE	Trypanosoma brucei.				
ORGANISM	Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.				
REFERENCE	1 (bases 1 to 27)				
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.				
TITLE	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk				
JOURNAL	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 (Gurrat 10.1) was mechanically sheared to give a tight size distribution (~ 4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).				
COMMENT	Details of T. brucei sequencing at the Sanger Centre are available at <a href="http://www.sanger.ac.uk/Projects/T_brucei/">http://www.sanger.ac.uk/Projects/T_brucei/</a> .				
FEATURES	1 - 27				
source	/organism="Trypanosoma brucei"				
DEFINITION	/strain="TREU927"				
source	/db_xref="taxon:5691"				
DEFINITION	/clone="128c06"				
source	5 a 3 c 8 g 11 t				
BASE COUNT	.				
ORIGIN	7 a 12 c 2 g 7 t				
RESULTS	7				
LOCUS	AZ760461	AZ760461	28 bp	DNA	linear GSS 16-FEB-2001
DEFINITION	1M0054AC13F Mouse 10kb Plasmid UGCG1M library Mus musculus genomic clone UGC1M054C13 F, DNA sequence.				
VERSION	AZ760461	AZ760461			
KEYWORDS	house mouse.				
ORGANISM	Mus musculus.				
SOURCE	GSS.				
COMMENT	University of Utah Genome Center				
REFERENCE	ddunn@genetics.utah.edu				
AUTHORS	University of Utah				
TITLE	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
FEATURES	Source				
source	1 . 28				
DEFINITION	/organism="Mus musculus"				
source	/strain="C57BL/6J"				
DEFINITION	/db_xref="taxon:10090"				
source	/clone="UGCG1M054C13"				
DEFINITION	/clone_lib="Mouse 10kb plasmid UGCG1M library"				
source	/sex="Male"				
DEFINITION	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-				
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source	Location/Qualifiers				
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VERSION	AZ33903	AZ33903			
KEYWORDS	GSS.				
ORGANISM	house mouse.				
SOURCE	GSS.				
COMMENT	University of Utah Genome Center				
REFERENCE	ddunn@genetics.utah.edu				
AUTHORS	University of Utah				
TITLE	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
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source	Location/Qualifiers				
DEFINITION	1 . 28				
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source	Location/Qualifiers				
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DEFINITION	1M0054AC13F Mouse 10kb Plasmid UGCG1M library Mus musculus genomic clone UGC1M054C13 F, DNA sequence.				
VERSION	AZ760461	AZ760461			
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ORGANISM	Mus musculus.				
SOURCE	GSS.				
COMMENT	University of Utah Genome Center				
REFERENCE	ddunn@genetics.utah.edu				
AUTHORS	University of Utah				
TITLE	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
FEATURES	Source				
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LOCUS	AZ33903	AZ33903	29 bp	DNA	linear GSS 29-SEP-2001
DEFINITION	1M0045007R Mouse 10kb Plasmid UGCG1M library Mus musculus genomic clone UGC1M004504A01 R, DNA sequence.				
VERSION	AZ33903	AZ33903			
KEYWORDS	GSS.				
ORGANISM	house mouse.				
SOURCE	GSS.				
COMMENT	University of Utah Genome Center				
REFERENCE	ddunn@genetics.utah.edu				
AUTHORS	University of Utah				
TITLE	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
FEATURES	Source				
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DEFINITION	1M0045007R Mouse 10kb Plasmid UGCG1M library Mus musculus genomic clone UGC1M004504A01 R, DNA sequence.				
VERSION	AZ33903	AZ33903			
KEYWORDS	GSS.				
ORGANISM	house mouse.				
SOURCE	GSS.				
COMMENT	University of Utah Genome Center				
REFERENCE	ddunn@genetics.utah.edu				
AUTHORS	University of Utah				
TITLE	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
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source	Location/Qualifiers				
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ORIGIN	7 a 12 c 2 g 7 t				
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LOCUS	AZ33903	AZ33903	29 bp	DNA	linear GSS 29-SEP-2001
DEFINITION	1M0045007R Mouse 10kb Plasmid UGCG1M library Mus musculus genomic clone UGC1M004504A01 R, DNA sequence.				
VERSION	AZ33903	AZ33903			
KEYWORDS	GSS.				
ORGANISM	house mouse.				
SOURCE	GSS.				
COMMENT	University of Utah Genome Center				
REFERENCE	ddunn@genetics.utah.edu				
AUTHORS	University of Utah				
TITLE	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
FEATURES	Source				
source	1 . 28				</

ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.	SOURCE ORGANISM	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Muridae; Murinae; Mus. 1 (bases 1 to 29)
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.	REFERENCE AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
TITLE	Unpublished (2000)	JOURNAL	Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177	COMMENT	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177
COMMENT	Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0045 row: A column: 07 Seq primer: CACACGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 29.	FEATURES source	Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0535 row: M column: 12 Seq primer: CGTTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 29. Location/Qualifiers 1..29 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M035M12" /clone_idb="Mouse 10kb plasmid UUGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /note="Vector: PWD2Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://wwwjax.org/resources/documents/dnares/">http://wwwjax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 14732114 gb AF129072.1), a copy number inducible derivative of Plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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KEYWORDS	GSS, house mouse.	VERSION	A2433969.1	GI:10557982
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathini; Muridae; Murinae; Mus .	ORGANISM	Mus musculus		
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AUTHORS Dunn D., Aoyagi A., Barber M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre,S., Mahinoud, M., Meenin, E., Pederesen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.	AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahinoud, M., Meenin, E., Pederesen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.		
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL Unpublished (2000)	JOURNAL	Unpublished (2000)		
COMMENT Contact: Robert B. Weiss	COMMENT	Contact: Robert B. Weiss		
University of Utah Genome Center	COMMENT	University of Utah Genome Center		
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	COMMENT	University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA		
Phone: 801 585 5606	COMMENT	Phone: 801 585 5606		
Fax: 801 585 7177	COMMENT	Fax: 801 585 7177		
Email: ddunngenetics.utah.edu	COMMENT	Email: ddunngenetics.utah.edu		
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gili47321141gb AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	FEATURES	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gili47321141gb AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
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ORIGIN 4 c	BASE COUNT	3 c		
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10 g	ORIGIN	11 t		
9 t	ORIGIN			
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0; Mismatches 5;	Query Match	0; Mismatches 0;	Gaps 0;	Gaps 0;
Indels 0;	Query Match	Indels 0;		
Gaps 0;	Query Match	Gaps 0;		
•	Query Match	•		
Query 2448 gaaggcttatgtcaagtgtcaagat 2471	Query	1553 tcagaataaaaccaatgg 1571		
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 VERSION D25863.1  
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 SOURCE  
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 Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K.  
 Global analysis of gene expression in colon mucosa: a large scale  
 random cDNA sequencing analysis  
 Unpublished (1994)  
 Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K.  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES Location/Qualifiers  
 1..27  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Cml743"  
 /clone="Human colon mucosa"  
 /note="Adult male, tissue-type = colon mucosa"  
 BASE COUNT 13 a 9 AACACATGGTATTCCAAA 27  
 ORIGIN

Query Match 0.6%; Score 15.8%; DB 10; Length 27;  
 Best Local Similarity 89.5%; Pred. No. 1.7e+07; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2;

Qy 2508 aacacaatgtactaaaa 2526  
 : Db 9 AACACATGGTATTCCAAA 27

RESULT 14  
 AZ799395  
 LOCUS AZ799395  
 DEFINITION 2M0056N16R Mouse 10Kb plasmid UGCGLM library Mus musculus genomic  
 clone UGCG2M0056N16 R, DNA sequence.

Qy 330 cagcactactgacaaatgtggcccaaq 356  
 Db 28 CTGCACTACCACATCAGTGCTCAAGS 2

BASE COUNT 5 a 10 g 8 t  
 ORIGIN

Query Match 0.6%; Score 15.8%; DB 9; Length 28;  
 Best Local Similarity 74.1%; Pred. No. 1.7e+07; Indels 7; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 7;

Qy 330 cagcactactgacaaatgtggcccaaq 356  
 Db 28 CTGCACTACCACATCAGTGCTCAAGS 2

RESULT 14  
 AZ799395  
 LOCUS AZ799395  
 DEFINITION 2M0056N16R Mouse 10Kb plasmid UGCGLM library Mus musculus genomic  
 clone UGCG2M0056N16 R, DNA sequence.

Qy 330 cagcactactgacaaatgtggcccaaq 356  
 Db 28 CTGCACTACCACATCAGTGCTCAAGS 2

BASE COUNT 5 a 10 g 8 t  
 ORIGIN

Query Match 0.6%; Score 15.8%; DB 10; Length 27;  
 Best Local Similarity 89.5%; Pred. No. 1.7e+07; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2;

Qy 2508 aacacaatgtactaaaa 2526  
 : Db 9 AACACATGGTATTCCAAA 27

RESULT 13  
 AI826975/c  
 LOCUS AI826975  
 DEFINITION wks5a12.x1 NCI-CGAP\_Pr22 Homo sapiens cDNA clone IMAGE:2419294\_3,  
 similar to SW:AR34\_HUMAN O15144 ARP2/3 COMPLEX 34 KD SUBUNIT ; ,  
 mRNA sequence.  
 AI826975  
 AI826975.1 GI:5447646  
 EST.  
 KEYWORDS human  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
 1 (bases 1 to 28)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/nicicgap.  
 Unpublished (1997)  
 CONTACT: Robert Straussberg, Ph.D.  
 Email: cgapbs@nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/obrp/image/image.html](http://www.bio.llnl.gov/obrp/image/image.html)

Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

FEATURES Location/Qualifiers  
 source

ACCESSION D25863  
 VERSION D25863.1  
 EST. GI:500531  
 KEYWORDS human  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
 1 (bases 1 to 27)  
 Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K.  
 Global analysis of gene expression in colon mucosa: a large scale  
 random cDNA sequencing analysis  
 Unpublished (1994)  
 Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K.  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES Location/Qualifiers  
 1..27  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Cml743"  
 /clone="Human colon mucosa"  
 /note="Adult male, tissue-type = colon mucosa"  
 /db\_xref="taxon:10090"  
 /clone="UGCG2M0056N16"  
 /clone\_1\_id="Mouse 10Kb plasmid UGCGLM library"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
<http://wwwjax.org/resources/documents/dnares/>. The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWb12 (gi|472114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.<sup>11</sup>

BASE COUNT 0 a 14 c 13 g 1 t

ORIGIN 10 a 5 c 11 g 3 t

```
Query Match 0.6%; Score 15.8; DB 12; Length 28;
Best Local Similarity 74.1%; Prod. No. 1.7e+07;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 17 ggcggggggggactccatccctggccc 43
Db 2 GGGGGGGGGGGCCCTCCCCCCCCCCC 28
```

#### RESULT 15

LOCUS AZ475726 29 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0294F02F Mouse 10kb Plasmid UGCI1M library Mus musculus genomic
clone UGCI1M0294F02 F, DNA sequence.

#### ACCESSION AZ475726

#### VERSION AZ475726.1

#### KEYWORDS GI:10633851

#### SOURCE GSS.

#### ORGANISM Mus musculus

#### Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

#### 1 (bases 1 to 29)

#### Dunn,D., Longacre,S., Mahmood,M., Meinen,E., Peersen,T., Reilly

#### M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

#### and Wright,D., Weiss,R.

#### Mouse whole genome scaffolding with paired end reads from 10kb

#### plasmid inserts

#### Unpublished (2000)

#### Contact: Robert B. Weiss

#### University of Utah Genome Center

#### Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

#### 84112, USA

#### Tel: 801 585 5606

#### Fax: 801 585 7177

#### Email: ddunn@genetics.utah.edu

#### Insert Length: 10000 Std Error: 0.00

#### Plate: 024 row: F column: 02

#### Seq primer: CGTGTAAACGACGCCAGT

#### Class: Plasmid ends

#### High quality sequence stop: 29.

#### Location/Qualifiers

#### 1..29

#### /organism="Mus musculus"

#### /strain="C57BL/6J"

#### /db\_xref="taxon:10090"

#### /clone="UGCIM0294F02"

#### /sex="Male"

#### /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-

#### /note="Vector: PWDA2ny; Purified genomic DNA from M.

#### musculus C57BL/6J (male) was obtained from the Jackson

#### Laboratory Mouse DNA Resource

#### (http://wwwjax.org/resources/documents/dnares/). The DNA

#### was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 Polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWb12 (gi|472114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.<sup>11</sup>

BASE COUNT 10 a 5 c 11 g 3 t

ORIGIN 10 a 5 c 11 g 3 t

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Query Match 0.6%; Score 15.8; DB 12; Length 29;
Best Local Similarity 74.1%; Prod. No. 1.7e+07;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy 17 actcgccaaaggtaagcaggagaataa 1741
Db 2 AATGCCAGGGGATGAAGCAGAGTAA 28

Search completed: September 7, 2002, 01:05:00
Job time: 5716 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 02:04:54 ; Search time 4642.65 seconds  
(without alignments)  
17434.836 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaatccggcacgagcgccg.....9gtcttgggtacgagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 524256

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:  
 1: qb\_ba:\*
 2: qb\_hhg:\*
 3: qb\_ln:\*
 4: qb\_lom:\*
 5: qb\_ov:\*
 6: qb\_pat:\*
 7: qb\_pn:\*
 8: qb\_pl:\*
 9: qb\_pr:\*
 10: qb\_ro:\*
 11: qb\_sts:\*
 12: qb\_sy:\*
 13: qb\_un:\*
 14: qb\_vl:\*
 15: em\_ba:\*
 16: em\_fun:\*
 17: em\_hum:\*
 18: em\_in:\*
 19: em\_mu:\*
 20: em\_on:\*
 21: em\_or:\*
 22: em\_ov:\*
 23: em\_pat:\*
 24: em\_ph:\*
 25: em\_pl:\*
 26: em\_ro:\*
 27: em\_sts:\*
 28: em\_un:\*
 29: em\_ii:\*
 30: em\_htg\_hum:\*
 31: em\_htg\_inv:\*
 32: em\_htg\_other:\*
 33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
	%	Query Match Length	DB ID	Description
BASE COUNT	5	a	/organism="unknown"	
ORIGIN	8	c	9	g
FEATURES	1	.26		
REFERENCE	1	(bases 1 to 26)		
AUTHORS		Chantrey,D.H., Hoekstra,M.F. and Holtzman,D.A.		
TITLE		Lipid kinase		
JOURNAL		Patent: US 5858733-A 9 12-JAN-1999;		
SOURCE		Location/Qualifiers		
RESULT	1			
LOCUS	AR028693/c	AR028693	Sequence 9 from patent US 5858733.	26 bp
DEFINITION			DNA	
ACCESSION	AR028693		linear	
VERSION	ARU28693.1	GI:5940666	PAT	29-SEP-1999
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
UNCLASSIFIED				
REFERENCE	1	(bases 1 to 26)		
AUTHORS		Chantrey,D.H., Hoekstra,M.F. and Holtzman,D.A.		
TITLE		Lipid kinase		
JOURNAL		Patent: US 5858733-A 9 12-JAN-1999;		
FEATURES		Location/Qualifiers		
SOURCE	1	.26		
BASE COUNT	5	a	/organism="unknown"	
ORIGIN	8	c	9	g
FEATURES	4	t		
SUMMARIES				

Query Match Length DB ID Description

Best Local Similarity 0.7%; Score 26; DB 6; Length 26;  
Pred. No. 1.7e+06;





source 1. .21  
 /organism="unknown"  
 BASE COUNT 5 a 6 c 5 g 5 t

---

RESULT 14  
 AR086502  
 LOCUS AR086502 Sequence 7 from patent US 5985589.  
 DEFINITION Sequence 7 from patent US 5985589.  
 ACCESSION AR086502  
 VERSION AR086502.1 GI:10013268  
 KEYWORDS Unknown  
 SOURCE Unknown  
 ORGANISM Unknown  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
 TITLE Lipid kinase  
 JOURNAL Patent: US 5985589-A 7 16-Nov-1999;  
 FEATURES Location/Qualifiers  
 source 1. .21  
 BASE COUNT 5 a 6 c 5 g 5 t

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Query Match 0.5%; Score 21; DB 6; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2557 catgtcgaccctgcagatgt 2577  
 Db 1 CATGCTGACCCCTGCAGATGT 21

---

RESULT 12  
 AR028692/c  
 LOCUS AR028692 Sequence 8 from patent US 5858753.  
 DEFINITION Sequence 8 from patent US 5858753.  
 ACCESSION AR028692  
 VERSION AR028692.1 GI:5940665  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
 TITLE Lipid kinase  
 JOURNAL Patent: US 5858753-A 8 12-JAN-1999;  
 FEATURES Location/Qualifiers  
 source 1. .21  
 /organism="unknown"  
 BASE COUNT 4 a 9 c 4 g 4 t

---

Query Match 0.5%; Score 21; DB 6; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2899 cggagatgtggcagctgtt 2919  
 Db 21 CCGAGAGTGGCAGCTGT 1

---

RESULT 13  
 AR028699/c  
 LOCUS AR028699 Sequence 16 from patent US 5858753.  
 DEFINITION Sequence 16 from patent US 5858753.  
 ACCESSION AR028699  
 VERSION AR028699.1 GI:5940672  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
 TITLE Lipid kinase  
 JOURNAL Patent: US 5858753-A 8 16-Nov-1999;  
 FEATURES Location/Qualifiers  
 source 1. .21  
 BASE COUNT 4 a 9 c 4 g 4 t

---

Query Match 0.5%; Score 21; DB 6; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2899 cggagatgtggcagctgtt 2919  
 Db 21 CCGAGAGTGGCAGCTGT 1

---

Query Match 0.5%; Score 21; DB 6; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2712 tcacaaggacatggcag 2732  
 Db 21 TCAACAGAGCACATGGCAG 1

---

Search completed: September 7, 2002, 05:22:56  
 Job time: 11882 sec



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PT signalling and in carcinogenesis  
XX

PS Example 1; Page 11; 53pp; English.

XX 2 Antisense gene-specific oligonucleotide primers (see AAV3:1345 and  
CC AAV3:146) respectively comprise a primary RACE primer and a nested  
CC RACE primer, and are based on the 5' end of M928, a cDNA clone  
CC obtained from human macrophage cDNA by PCR amplification (see  
CC AAV3:143-44). They were used to amplify 5' sequences of human  
CC phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic  
CC subunit cDNA, using leucocyte cDNA as template. Amplified products  
CC were used as templates in a nested PCR and the reamplified products  
CC were then analyzed using probes (see AAV3:147-48) specific for p110  
CC delta. The specific 5' RACE PCR products were combined with  
partial clones #249 and M928 to produce a composite cDNA (AAV3:140)  
CC sequence coding for human PI 3-kinase p110 delta catalytic subunit  
(see AAV3:8570). This can be used to develop products for modulating  
CC PI 3-kinase activity in immune system signalling and in  
CC carcinogenesis.  
XX

SO Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;

Query Match 0.7%; Score 26; DB 19; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 1500 gggaaacctgccttacatgtggcc 1525

Db 26 GGGAACGCTGCCCTACATGTGGCC 1

RESULT 2  
AAV15937/c  
ID .AAV15937 standard; DNA; 26 BP.

XX AAV15937;  
DT 14-MAY-1999 (first entry)

DE PCR primer used to amplify cDNA sequence encoding p110-delta.  
XX Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;  
KW PI3-Kinase mediated signalling; immune system; phosphatidylinositol;  
KW PI; kinase activity; PCR primer; ss.  
OS Synthetic.  
OS Homo sapiens.  
XX US5882910-A.  
XX 16-MAR-1999.  
XX PF 25-NOV-1997; 97US-0977871.  
XX PR 25-NOV-1996; 96US-0777405.  
XX PA (ICOS-) ICOS CORP.  
XX PI Chantry DH, Hoekstra MF, Holtzman DA;  
XX DR WPI; 1999-214067/18.

XX Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
PT enzymes - useful as antigens and for identifying agents which  
PT modulate the enzymes kinase activity or binding to substrates and  
PT co-factors  
XX Example 1; Columns 6; 22pp; English.

XX PCR primers AAV15937-38 were used to isolate cDNA encoding a catalytic  
CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase  
XX

CC enzyme which is involved in PI3-Kinase mediated signalling in the  
CC immune system. p110 delta phosphorylates phosphatidylinositol (PI),  
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).

CC p110-delta may be used as an antigen in the production of  
CC antibodies (using standard techniques) which may be used, for  
CC example, to modulate (ie blocking, inhibiting or stimulating) the  
CC binding between p110-delta and its binding partner. P110-delta may  
CC also be used in assays to identify modulators which inhibit or  
CC activate its kinase activity.

SO Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;

Query Match 0.7%; Score 26; DB 20; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 1500 gggaaacctgccttacatgtggcc 1525

Db 26 GGGAACGCTGCCCTACATGTGGCC 1

RESULT 3  
AAZ32887/c  
ID AAZ32887 standard; DNA; 26 BP.

XX AAZ32887;

DT 09-FEB-2000 (first entry)  
DE Human PI 3-Kinase-related catalytic subunit p110-delta PCR primer #9.  
XX

KW lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;  
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;  
KW cellular response; growth; differentiation; apoptosis;  
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;  
KW Interleukin-2; IL-2; Prostaglandin; T cell; Leukocyte signalling; modulator;  
KW antagonist; agonist; treatment; disorder; cell growth;  
KW cell differentiation; immune activation; PCR; primer; ss.  
OS Synthetic.  
OS Homo sapiens.  
XX US5985589-A.  
XX PD 16-NOV-1999.  
XX PF 06-JAN-1999; 99US-0225951.  
XX PR 25-NOV-1997; 97US-0977871.  
XX PR 25-NOV-1996; 96US-0777405.  
XX PA (ICOS-) ICOS CORP.  
XX PI Holtzman DA, Hoekstra MF, Chantry DH;  
XX DR WPI; 2000-012785/01.

XX Identifying modulators of lipid kinase subunit p110delta activity -  
XX PS Example 1; column 6; 22pp; English.

XX This sequence represents human p110-delta PCR primer #9, used in the  
CC generation of a full-length cDNA (AAZ32887) encoding a novel lipid  
CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol  
CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a  
CC membrane-locating p85 subunit and a catalytic p110 subunit. These  
CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
CC are differentially expressed, and p110 has to date three isoforms  
CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
the 3' hydroxyl of the inositol ring with the primary product of PI

CC 3'-kinase-mediated phosphorylation being phosphatidylinositol (3', 4', 5') triphosphate (PIP3). PI 3-kinase is activated by interaction with G proteins and PI 3-kinase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and apoptosis. The downstream targets of the phosphorylated lipids generated following PI 3-kinase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated by PIP3 in vitro. PI 3-kinase also appears to be involved in certain aspects of leukocyte activation, such as interleukin-2 (IL-2) production in T cells, and leukocyte signalling through G-protein coupled receptors. pI10-delta, or nucleotides encoding it, may be used to identify modulators of pI10-delta and/or PI 3-kinase activity. These may be useful in the treatment of disorders associated with cell growth, cell differentiation, apoptosis or immune activation.

Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;

Query Match 0.7%; Score 26; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+04; Mismatches 0; Indels 0; Gaps 0;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1500 gggaacgcttcccttacatgtggccc 1525  
 Db 26 GGGAAACGCTGCCTCTACATGGGCC 1

RESULT 4

AAV31346/c  
 ID AAV31346 standard; DNA; 25 BP.  
 AC AAV31346;  
 XX

DE 12-OCT-1998 (first entry)

XX DE Phosphatidylinositol 3-kinase pI10 delta subunit RACE primer.  
 KW KW Phosphatidylinositol 3-kinase; pI10 delta; human; immune system;  
 KW carcinogenesis; diagnosis; PCR; primer; RACE; ss.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX PN WO9823760-A1.  
 XX PR PD 04-JUN-1998.  
 XX PR 25-NOV-1997; 97WO-US21655.  
 XX PR 25-NOV-1996; 96US-0777405.  
 XX PA (ICOS-) ICOS CORP.  
 XX PI Chantry DH, Hoekstra MF, Holtzman DA;  
 XX DR WPI; 1998-322736/28.

XX PT New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system  
 PT signalining and in carcinogenesis  
 XX PS Example 1; Page 11; 53pp; English.

CC 2. Antisense gene-specific oligonucleotide primers (see AAV31345 and AAV31346) respectively comprise a primary RACE primer and a nested RACE primer, and are based on the 5' end of M#928, a cDNA clone obtained from human macrophage cDNA by PCR amplification (see AAV31343-44). They were used to amplify 5' sequences of human phosphatidylinositol 3-kinase (PI 3-kinase) pI10 delta catalytic subunit cDNA, using leucocyte cDNA as template. Amplified products were used as templates in a nested PCR and the reamplified products were then analysed using probes (see AAV31347-48) specific for pI10 delta. The specific 5' RACE PCR products were combined with

CC partial clones #249 and M#928 to produce a composite cDNA (AAV31340) sequence coding for human PI 3-kinase pI10 delta catalytic subunit (see AAW5870). This can be used to develop products for modulating PI 3-kinase activity in immune system signalling and in carcinogenesis.

CC Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;  
 SQ

Query Match 0.6%; Score 25; DB 20; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+04; Mismatches 0; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1435 ggccgactgcgccatgcctggggc 1459  
 Db 25 GCGGACTGCCCATGCGCGGCC 1

RESULT 5

AAV15938/c  
 ID AAV15938 standard; DNA; 25 BP.  
 AC AAV15938;  
 XX

DE 14-MAY-1999 (first entry)

XX DE PCR Primer used to amplify cDNA sequence encoding pI10-delta.  
 KW KW Catalytic subunit; pI10-delta; phosphatidylinositol 3-kinase; PI3-kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; PCR primer; ss.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX PN US5802910-A.  
 XX PD 16-MAR-1999.  
 XX PF 25-NOV-1997; 97US-0977871.  
 XX PR 25-NOV-1997; 97US-0977871.  
 XX PR 25-NOV-1996; 96US-0777405.  
 XX PA (ICOS-) ICOS CORP.  
 XX PI Chantry DH, Hoekstra MF, Holtzman DA;  
 XX DR WPI; 1999-214067/18.

XX PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and co-factors  
 XX PS Example 1; Columns 6; 22pp; English.

CC PCR Primers AAV15937-38 were used to isolate cDNA encoding a catalytic subunit (pI10-delta), derived from a phosphatidylinositol 3-kinase enzyme which is involved in PI3-kinase mediated signalling in the immune system. pI10-delta phosphorylates phosphatidylinositol (PI), and derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC pI10-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (i.e blocking, inhibiting or stimulating) the binding between pI10-delta and its binding partner. pI10-delta may also be used in assays to identify modulators which inhibit or activate its kinase activity.  
 CC Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;  
 SQ

Query Match 0.6%; Score 25; DB 20; Length 25;



			ID	AAV31348_C
XX			XX	Homo sapiens.
XX			XX	US5882910-A.
AC			PN	
AAV31348;			XX	
XX			PD	16-MAR-1999.
DT	12-OCT-1998	(first entry)	XX	
XX			PR	25-NOV-1997; 97US-0977871.
DE	Phosphatidylinositol 3-kinase p110 delta subunit probe.		XX	
KW	Phosphatidylinositol 3-kinase; p110 delta; human; immune system; carcinogenesis; diagnosis; probe; ss.		PR	25-NOV-1996; 96US-0777405.
KW			XX	
OS	Synthetic.		PA	(ICOS-) ICOS CORP.
XX	Homo sapiens.		XX	
XX	W09823760-A1.		PI	Chantry DH, Hoekstra MF, Holtzman DA;
PN			XX	
XX	04-JUN-1998.		DR	WPI; 1999-214067/18.
PD			XX	
XX	25-NOV-1997; 97US-0977871.		PT	Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and co-factors
PR	25-NOV-1996; 96US-0777405.		PT	
XX			XX	
PA	(ICOS-) ICOS CORP.		PS	Example 1: Columns 7; 22pp; English.
XX			CC	Probes AAX15939-40 were used to isolate cDNA encoding a catalytic subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase enzyme which is involved in PI3-Kinase mediated signalling in the immune system. p110-delta phosphorylates phosphatidylinositol (PI), and derivatives of it at the 3'-hydroxyl of the inositol ring). p110-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (ie blocking, inhibiting or stimulating) the binding between p110-delta and its binding partner. p110-delta may also be used in assays to identify modulators which inhibit or activate its kinase activity.
PT	New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system signalling and in carcinogenesis		CC	
PT			CC	
PT			CC	
PS	Example 1, Page 11; 53pp; English.		CC	
XX	2. Oligonucleotide probes (see AAV31347 and AAV31348) are specific for the human phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic subunit. They were used in Southern blotting to screen clones obtained from 5' RACE and nested PCR amplifications of human leukocyte cDNA (see AAV31345-46). Specific 5' RACE PCR products were identified, and were combined with partial clones #49 and M#98 to produce a composite cDNA (AAV31340) sequence coding for human PI 3-kinase p110 delta catalytic subunit (see AAW58570). This can be used to develop products for modulating PI 3-kinase activity in immune system signalling and in carcinogenesis.		CC	
CC			CC	
CC			CC	
CC			CC	
SQ	Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;		SQ	Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;
RESULT	0.6%; Score 23; DB 19; Length 23;		RESULT	0.6%; Score 23; DB 20; Length 23;
9	Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 23; Conservative 0; Indels 0; Gaps 0;		9	Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 23; Conservative 0; Indels 0; Gaps 0;
Matches			Matches	
23			23	
Qy	1132 ctctgtgtccctgtggccctgg 1154		Qy	1149 ccctcgagccgcgcgtccgcata 1171
Db	23 CTCCTGTCGCCTGGTCCCTGG 1		Db	23 CCCCTGAGCACCGTTCGGCATC 1
RESULT	10		RESULT	10
	AAX15940/c			AAX15940/c
	ID AAX15940 standard; DNA; 23 BP.			ID AAX15940 standard; DNA; 23 BP.
AC			XX	
AAV31348;			AC	AAX15940;
XX			XX	
AC	AAX15939;		DT	14-MAY-1999 (first entry)
XX			XX	
AC	14-MAY-1999 (first entry)		DE	probe used to isolate cDNA sequence encoding p110-delta.
XX			XX	
DE	Probe used to isolate cDNA sequence encoding p110-delta.		KW	Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase; PI3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; probe; ss.
DE			KW	
XX			XX	Synthetic.
AC			OS	
XX			OS	Homo sapiens.
AC			XX	
AAV31348;			PN	US5882910-A.
XX			XX	
AC			PD	16-MAR-1999.
AAV31348;			XX	
XX			PR	25-NOV-1997; 97US-0977871.
XX			XX	
DE	Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase; PI3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; probe; ss.		PR	25-NOV-1997; 97US-0977871.
XX			PR	25-NOV-1996; 96US-0777405.
OS	Synthetic.		OS	

XX  
 XX (ICOS-) ICOS CORP.  
 PA  
 XX PT  
 PT Chantry DH, Hoekstra MF, Holtzman DA;  
 XX DR  
 WPI; 1999-214067-1B.

XX Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and co-factors

XX PS Example 1; Column 7; 22pp; English.

XX Probes AXI15939-40 were used to isolate cDNA encoding a catalytic subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase enzyme which is involved in PI3-Kinase mediated signalling in the immune system. p110-delta phosphorylates phosphatidylinositol (PI), and derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC p110-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (ie blocking, inhibiting or stimulating) the binding between p110-delta and its binding partner, p110-delta may also be used in assays to identify modulators which inhibit or activate its kinase activity.

CC Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;

CC Query Match 0.6%; Score 23; DB 20; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;

CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1132 ctctgtatccctgtggcccttg 1154

CC Db 23 CCTCTGGTCCCTGTCGCCCTGG 1

CC AC

CC RESULT 11

CC AAZ3289/C

CC DT 09-FEB-2000 (first entry)

CC DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #11.

CC XX

CC Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PKC; leukocyte activation; interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator; antagonist; agonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.

CC OS Synthetica.

CC OS Homo sapiens.

CC PN US5985589-A.

CC XX 16-NOV-1999.

CC PF 06-JAN-1999; 99US-0225951.

CC PR 25-NOV-1997; 97US-0977871.

CC XX 25-NOV-1996; 96US-0777405.

CC PA (ICOS-) ICOS CORP.

CC XX PI Holtzman DA, Hoekstra MF, Chantry DH;

DR WPI; 2000-012785/01.

XX PS Identifying modulators of lipid kinase subunit p110delta activity - Example 1; Column 7; 22pp; English.

CC This sequence represents human p110-delta PCR primer #11, used in the generation of a full-length cDNA (AAZ32882) encoding a novel lipid kinase catalytic subunit, p110-delta, related to phosphatidylinositol 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a membrane-localising p85 subunit and a catalytic p110 subunit. These subunits both have isoforms; p85 has two isoforms (alpha and beta) which are differentially expressed, and p110 has to date three isoforms (alpha, beta and gamma) that vary in their ability to associate with p85.

CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at the 3' hydroxyl of the inositol ring with the primary product of PI 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5) triphosphate (PIP3). PI 3-kinase is activated by interaction with G proteins and PI 3-kinase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and apoptosis. The downstream targets of the phosphorylated lipids generated following PI 3-kinase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated by PIP3 in vitro. PI 3-kinase also appears to be involved in certain aspects of leukocyte activation such as interleukin-2 (IL-2) production in T cells, and leukocyte signalling through G-protein coupled receptors. p110-delta, or nucleotides encoding it, may be used to identify modulators of p110-delta and/or PI 3-kinase activity. These may be useful in the treatment of disorders associated with cell growth, cell differentiation, apoptosis or immune activation.

CC XX Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;

CC Query Match 0.6%; Score 23; DB 21; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;

CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1149 ccctgaggcaggcggttccgatc 1171

CC Db 23 CCCTGGAGCACCGTTCGGCARTC 1

CC AC

CC RESULT 12

CC AAZ3289/C

CC DT 09-FEB-2000 (first entry)

CC DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #12.

CC XX

CC Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PKC; leukocyte activation; interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator; antagonist; agonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.

CC OS Synthetic.

CC OS Homo sapiens.

CC PN US5985589-A.

CC XX 16-NOV-1999.

CC PF 06-JAN-1999; 99US-0225951.

CC PR 25-NOV-1997; 97US-0977871.

CC XX 25-NOV-1996; 96US-0777405.

XX	PA	(ICOS-) ICOS CORP.
XX	PI	Chantry DH, Hoekstra MF, Holtzman DA;
XX	XX	Holtzman DA, Hoekstra MF, Chantry DH;
XX	DR	WPI; 2000-012785/01.
XX	PT	Identifying modulators of lipid kinase subunit p110delta activity -
XX	PS	Example 1; Column 7; 22pp; English.
CC	CC	This sequence represents human p110-delta PCR primer #12, used in the generation of a full-length cDNA (AAZ22882) encoding a novel lipid kinase catalytic subunit, p110-delta, related to phosphatidylinositol 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a membrane-localising p85 subunit and a catalytic p110 subunit. These subunits both have isoforms; p85 has two isoforms (alpha and beta) which are differentially expressed, and p110 has to date three isoforms (alpha, beta and gamma), that vary in their ability to associate with p85. PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at the 3' hydroxyl of the inositol ring with the primary product of PI 3-kinase-mediated phosphorylation being phosphatidylinositol (3,4, 5) triphosphate (PIP3). PI 3-kinase is activated by interaction with G proteins and PI 3-kinase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and apoptosis. The downstream targets of the phosphorylated lipids generated following PI 3-kinase activation have not yet been well characterised, although some isoforms of protein kinase C (PKC) are directly activated by PIP3 or may be involved in certain aspects of leukocyte activation, such as interleukin-2 (IL-2) production in T cells, and leukocyte signalling through G-protein coupled receptors. p110-delta, or nucleotides encoding it, may be used to identify modulators of p110-delta and/or PI 3-kinase activity. These may be useful in the treatment of disorders associated with cell growth, cell differentiation, apoptosis or immune activation.
CC	CC	Example 1; Page 12; 53pp; English.
CC	CC	This 3' primer was used with a 5' primer (see AAV31349) in the PCR amplification of 5 RACE PCR products (see AAU31345-46) of human leucocyte cDNA. The 5' primer includes a 5' BamHI site and sequences that code for a FLAG peptide (see AAU55571), which is recognised by the M2 anti-FLAG monoclonal antibody. The PCR product was combined with restriction fragments of partial clones #249 and #M#928 to produce a full-length cDNA (see AAU31347) for the p110 delta catalytic subunit (see AAU5870) of human phosphatidylinositol 3-kinase (PI 3-kinase). This was incorporated into expression vector pCMV3, and FLAG-tagged p110 delta was expressed in transfected COS cells. p110 delta can be used to develop products for modulating PI 3-kinase activity in immune system signalling and in carcinogenesis.
CC	CC	Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
CC	CC	Query Match 0.6%; Score 23; DB 21; Length 23; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	CC	Qy 1132 ccgtgttcccccgtggccctgg 1154 Db 23 CTCGTGTCGCCCTGGCTGG 1
XX	XX	Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
XX	XX	Query Match 0.6%; Score 22; DB 19; Length 22; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	XX	Qy 1501 ggaacgctgcctcacatqgg 1522 Db 22 GGAAGCTGCCTCATGAGGG 1
XX	XX	RESULT 13
AAV31350/CC	ID	RESULT 14
AAV31350 standard; DNA; 22 BP.	ID	AXA15942/C
XX	ID	AAX15942 standard; DNA; 22 BP.
AC	XX	XX
AAV31350;	AC	AAX15942;
XX	XX	DT 14-MAY-1999 (first entry)
DT 12-OCT-1998 (first entry)	DE	PCR primer used to amplify cDNA sequence encoding p110-delta.
XX	KW	Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase; PI3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; PCR primer; ss.
DE Phosphatidylinositol 3-kinase p110 delta subunit primer.	KW	OS Synthetic.
XX	OS	OS Homo sapiens.
XX	OS	XX
OS Synthetic.	PN	US5882910-A.
OS Homo sapiens.	XX	XX
PN WO9823760-A1.	PD	16-MAR-1999.
XX	XX	XX
XX	PR	25-NOV-1997; 97US-0977871.
OS Synthetica.	PR	25-NOV-1997; 97US-0977871.
OS Homo sapiens.	PR	25-NOV-1996; 96US-0777405.
PN	XX	XX
XX	PA	(ICOS-) ICOS CORP.
XX	XX	XX
PD 04-JUN-1998.	PI	Chantry DH, Hoekstra MF, Holtzman DA;
XX	DR	WPI; 1995-214067/18.
PF 25-NOV-1997; 97WO-US21655.	XX	XX
PR 25-NOV-1996; 96US-0777405.	PT	Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and PT co-factors
XX	PT	(ICOS-) ICOS CORP.

XX  
 PS Example 1; Columns 7; 22pp; English.  
 XX  
 CC PCR primers AAX15941-42 were used to isolate cDNA encoding a catalytic  
 CC subunit (p110-delta), derived from a phosphatidylinositol 3 kinase  
 CC enzyme which is involved in PI3-kinase mediated signalling in the  
 CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),  
 CC and derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC p110-delta may be used as an antigen in the production of  
 CC antibodies (using standard techniques) which may be used, for  
 CC example, to modulate (ie blocking, inhibiting or stimulating) the  
 CC binding between p110-delta and its binding partner. p110-delta may  
 CC also be used in assays to identify modulators which inhibit or  
 CC activate its kinase activity.

Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;

Query Match 0.6%; Score 22; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 ggaaacctggcccttacatgtgg 1522  
 Db 22 GGAAACGGTGCCTCTACATGTGG 1

RESULT 15  
 AAZ32892/C  
 ID AAZ32892 standard; DNA; 22 BP.  
 XX  
 AC AAZ32892;  
 AC  
 XX DT 09-FEB-2000 (first entry)  
 XX DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #14.  
 XX  
 KW LIPID KINASE; CATALYTIC; SUBUNIT; p110-delta; PI 3-KINASE;  
 KW PHOSPHATIDYLINOSITOL 3-KINASE; HETEROODIMERIC; ISOFORM; PHOSPHORYLATION;  
 KW PHOSPHATIDYLINOSITOL (3, 4, 5) TRIPHOSPHATE; PIP3; ACTIVATION; G PROTEIN;  
 KW CELLULAR RESPONSE; GROWTH; DIFFERENTIATION; APOPTOSIS;  
 KW PHOSPHORYLATED LIPID; PROTEIN KINASE C; PRKC; LEUKOCYTE ACTIVATION;  
 KW INTERLEUKIN-2; IL-2; PRODUCTION; T CELL; LEUKOCYTE SIGNALING; MODULATOR;  
 KW ANTAGONIST; AGONIST; TREATMENT; DISORDER; CELL GROWTH;  
 KW CELL DIFFERENTIATION; IMMUNE ACTIVATION; PCR; PRIMER; SS.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5985589-A.  
 XX  
 PD 16-NOV-1999.  
 XX  
 PF 06-JAN-1999; 99US-0225951.  
 XX  
 PR 25-NOV-1997; 97US-0977871.  
 PR 25-NOV-1996; 96US-077405.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Holtzman DA, Hoekstra MF, Chantry DH;  
 XX DR  
 XX WPI; 2000-012785/01.

Identifying modulators of lipid kinase subunit p110delta activity -

Example 1; Column 7; 22pp; English.

This sequence represents human p110-delta PCR primer #14, used in the generation of a full-length cDNA (AAZ32892) encoding a novel lipid kinase catalytic subunit, p110-delta, related to phosphatidylinositol 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a membrane-localising p85 subunit and a catalytic p110 subunit. These

CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
 CC are differentially expressed, and p110 has to date three isoforms (alpha,  
 CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
 CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
 CC the 3', hydroxyl of the inositol ring with the primary product of PI  
 CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)  
 CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G  
 CC proteins and PI 3-kinase activation is believed to be involved in a  
 CC range of cellular responses including cell growth, differentiation and  
 CC apoptosis. The downstream targets of the phosphorylated lipids generated  
 CC following PI 3-kinase activation have not been well characterised,  
 CC although some isoforms of protein kinase C (PKC) are directly activated  
 CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain  
 CC aspects of leukocyte activation, such as interleukin 2 (IL-2) production  
 CC in T cells, and leukocyte receptors. p110-delta or nucleotides encoding it, may be used to  
 CC identify modulators of p110-delta and/or PI 3-kinase activity. These may  
 CC be useful in the treatment of disorders associated with cell growth,  
 CC cell differentiation, apoptosis or immune activation.

Query Match 0.6%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 ggaaacctggcccttacatgtgg 1522  
 Db 22 GGAAACGGTGCCTCTACATGTGG 1

Search completed: September 7, 2002, 05:31:33  
 Job time: 8533 sec

Mon Sep 9 11:56:25 2002

us-10-049-743-1.rng

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GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 02:10:19 ; Search time 78.65 Seconds  
(without alignments)  
12080.234 Million cell updates/sec

Title: US-10-049-743-1

Perfect score: 3868

Sequence: 1 gaattccggcacgagcgccg . . . . . ggtcttgggtacgagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 403436

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents NA:\*

1: /cgn2\_6/ptodata/2/ina/\_5A\_COMB\_seq: \*  
2: /cgn2\_6/ptodata/2/ina/\_5B\_\_COMB\_seq: \*  
3: /cgn2\_6/ptodata/2/ina/\_6A\_COMB\_seq: \*  
4: /cgn2\_6/ptodata/2/ina/\_6B\_COMB\_seq: \*  
5: /cgn2\_6/ptodata/2/ina/\_PCRS\_\_COMB\_seq: \*  
6: /cgn2\_6/ptodata/2/ina/\_backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID

## Description

US-08-777-405A-9/

Sequence 9, Application US/08777405A

Patent No. 5858753

GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Holtzman, Douglas A

TITLE OF INVENTION: No. 5858753el Lipid Kinase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

STREET: 6300 Sears Tower/233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777,405A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5858753nd, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 2/866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-777-405A-9

Query Match 0.7%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1500 ggaaacctgtgcctcatatggcc 1525

## ALIGNMENTS

Sequence 10, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 15, Appl  
Sequence 16, Appl  
Sequence 17, Appl  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 20, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 23, Appl  
Sequence 24, Appl  
Sequence 25, Appl  
Sequence 26, Appl  
Sequence 27, Appl

Result No.	Score	Query	Match	Length	DB	ID	Description
1	26	0.7	26	2	US-08-777-405A-9		Sequence 9, Appl
2	26	0.7	26	2	US-08-777-871A-9		Sequence 9, Appl
3	26	0.7	26	2	US-09-225-951-9		Sequence 9, Appl
4	25	0.6	25	2	US-08-777-405A-10		Sequence 10, Appl
5	25	0.6	25	2	US-08-977-871A-10		Sequence 10, Appl
6	25	0.6	25	2	US-09-225-951-10		Sequence 10, Appl
7	23	0.6	23	2	US-08-777-405A-11		Sequence 11, Appl
8	23	0.6	23	2	US-08-777-405A-12		Sequence 11, Appl
9	23	0.6	23	2	US-08-977-871A-11		Sequence 11, Appl
10	23	0.6	23	2	US-08-977-871A-12		Sequence 11, Appl
11	23	0.6	23	2	US-09-225-951-11		Sequence 11, Appl
12	23	0.6	23	2	US-09-225-951-12		Sequence 12, Appl
13	22	0.6	22	2	US-08-777-405A-14		Sequence 14, Appl
14	22	0.6	22	2	US-08-977-871A-14		Sequence 14, Appl
15	22	0.6	22	2	US-09-225-951-14		Sequence 14, Appl
16	21	0.5	21	1	US-08-777-405A-7		Sequence 7, Appl
17	21	0.5	21	2	US-08-777-405A-8		Sequence 8, Appl
18	21	0.5	21	2	US-08-977-405A-16		Sequence 16, Appl
19	21	0.5	21	1	US-08-977-871A-7		Sequence 7, Appl
20	21	0.5	21	2	US-08-977-871A-8		Sequence 8, Appl
21	0.5	21	2	US-08-977-871A-16		Sequence 16, Appl	
22	0.5	21	2	US-08-225-951-7		Sequence 7, Appl	
23	0.5	21	2	US-09-225-951-8		Sequence 8, Appl	
24	0.5	21	2	US-09-225-951-16		Sequence 16, Appl	
25	0.5	21	3	US-09-357-070-3		Sequence 3, Appl	
26	0.5	20	3	US-09-357-070-8		Sequence 8, Appl	
27	0.5	20	3	US-09-357-070-9		Sequence 9, Appl	

Db 26 GGGAACGCTGCCCTACATGTGGCC 1

STATE: Illinois  
COUNTRY: USA

RESULT 2  
US-08-977-871A-9/c

; Sequence 9, Application US/08977871A  
; PATENT NO. 5882910

GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Hoekstra, Merl F.

TITLE OF INVENTION: No. 5882910el Lipid Kinase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

STREET: 6300 Sears Tower/233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/2225, 951

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: No. 585589and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-977-871A-9

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/777,405

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5882910and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-225-951-9

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/777-405A

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: 585873

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: 25-3856

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-225-951-9

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/777,405A

FILING DATE:

ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 35,302

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US-09-225-951-9

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ATTORNEY/AGENT INFORMATION:

NAME: 585873

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: 25-3856



MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/777,405A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 588753and, Greta E.  
 REFERENCE/DOCKET NUMBER: 35,302  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 US-08-777-055A-11

RESULT 8  
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 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1149 ccctggagccgcgttccgatc 1171  
 Db 23 CCCTGGAGCAGCGTCCGCATC 1

US-08-777-055A-12/C  
 Sequence 12, Application US/08/777405A  
 Patent No. 588753  
 GENERAL INFORMATION:  
 APPLICANT: Chantry, David  
 APPLICANT: Hoekstra, Merl F.  
 APPLICANT: Holtzman, Douglas A.  
 APPLICANT: Holtzman, Douglas A.  
 TITLE OF INVENTION: No. 5882910el Lupid Kinase  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
 STREET: 6300 Sears Tower/233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/977,871A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/777,405  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5882910and, Greta E.  
 REFERENCE/DOCKET NUMBER: 27866/33441  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 US-08-977-871A-11

RESULT 9  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1132 ctctggtcctgtgtccctgg 1154  
 Db 23 CCCTGGAGCAGCGTCCGCATC 1

Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1132 ctctggtcctgtgtccctgg 1154  
 Db 23 CCCTGGAGCAGCGTCCGCATC 1

Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1149 ccctggagccgcgttccgatc 1171  
 Db 23 CCCTGGAGCAGCGTCCGCATC 1

RESULT 10  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1149 ccctggagccgcgttccgatc 1171  
 Db 23 CCCTGGAGCAGCGTCCGCATC 1

Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1149 ccctggagccgcgttccgatc 1171  
 Db 23 CCCTGGAGCAGCGTCCGCATC 1

Sequence 12, Application US/08977871A  
 Patent No. 5882910  
 GENERAL INFORMATION:  
 APPLICANT: Chantry, David  
 APPLICANT: Hoeckstra, Merl F.  
 APPLICANT: Holtzman, Douglas A.  
 TITLE OF INVENTION: No. 5882910el Lipid Kinase  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
 STREET: 6300 Sears Tower/233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/225, 951  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/777, 405  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5882910and, Greta E.  
 REFERENCE/DOCKET NUMBER: 35, 302  
 TELECOMMUNICATION INFORMATION:  
 REFERENCE/DOCKET NUMBER: 27866/33441  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: other nucleic acid  
 US-08-977-871A-12  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: other nucleic acid  
 US-09-977-871A-12  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 Strands 1  
 Qy 1132 ctctgtgtccatgtggccctgg 1154  
 Db 23 CCTGIGGCCCTGGCCCCGG 1  
 RESULT 12  
 US-09-225-951-12/c  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 Strands 1  
 Qy 1149 ccctggaggccgcgtcccgatc 1171  
 Db 23 CCCTGGAGCACCCGTCGGCATC 1  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 Strands 1  
 Qy 1150 ||||||| 1151||| 1152||| 1153||| 1154||| 1155||| 1156||| 1157||| 1158||| 1159||| 1160||| 1161||| 1162||| 1163||| 1164||| 1165||| 1166||| 1167||| 1168||| 1169||| 1170||| 1171||| 1172||| 1173||| 1174||| 1175||| 1176||| 1177||| 1178||| 1179||| 1180||| 1181||| 1182||| 1183||| 1184||| 1185||| 1186||| 1187||| 1188||| 1189||| 1190||| 1191||| 1192||| 1193||| 1194||| 1195||| 1196||| 1197||| 1198||| 1199||| 1200||| 1201||| 1202||| 1203||| 1204||| 1205||| 1206||| 1207||| 1208||| 1209||| 1210||| 1211||| 1212||| 1213||| 1214||| 1215||| 1216||| 1217||| 1218||| 1219||| 1220||| 1221||| 1222||| 1223||| 1224||| 1225||| 1226||| 1227||| 1228||| 1229||| 1230||| 1231||| 1232||| 1233||| 1234||| 1235||| 1236||| 1237||| 1238||| 1239||| 1240||| 1241||| 1242||| 1243||| 1244||| 1245||| 1246||| 1247||| 1248||| 1249||| 1250||| 1251||| 1252||| 1253||| 1254||| 1255||| 1256||| 1257||| 1258||| 1259||| 1260||| 1261||| 1262||| 1263||| 1264||| 1265||| 1266||| 1267||| 1268||| 1269||| 1270||| 1271||| 1272||| 1273||| 1274||| 1275||| 1276||| 1277||| 1278||| 1279||| 1280||| 1281||| 1282||| 1283||| 1284||| 1285||| 1286||| 1287||| 1288||| 1289||| 1290||| 1291||| 1292||| 1293||| 1294||| 1295||| 1296||| 1297||| 1298||| 1299||| 1300||| 1301||| 1302||| 1303||| 1304||| 1305||| 1306||| 1307||| 1308||| 1309||| 1310||| 1311||| 1312||| 1313||| 1314||| 1315||| 1316||| 1317||| 1318||| 1319||| 1320||| 1321||| 1322||| 1323||| 1324||| 1325||| 1326||| 1327||| 1328||| 1329||| 1330||| 1331||| 1332||| 1333||| 1334||| 1335||| 1336||| 1337||| 1338||| 1339||| 1340||| 1341||| 1342||| 1343||| 1344||| 1345||| 1346||| 1347||| 1348||| 1349||| 1350||| 1351||| 1352||| 1353||| 1354||| 1355||| 1356||| 1357||| 1358||| 1359||| 1360||| 1361||| 1362||| 1363||| 1364||| 1365||| 1366||| 1367||| 1368||| 1369||| 1370||| 1371||| 1372||| 1373||| 1374||| 1375||| 1376||| 1377||| 1378||| 1379||| 1380||| 1381||| 1382||| 1383||| 1384||| 1385||| 1386||| 1387||| 1388||| 1389||| 1390||| 1391||| 1392||| 1393||| 1394||| 1395||| 1396||| 1397||| 1398||| 1399||| 1400||| 1401||| 1402||| 1403||| 1404||| 1405||| 1406||| 1407||| 1408||| 1409||| 1410||| 1411||| 1412||| 1413||| 1414||| 1415||| 1416||| 1417||| 1418||| 1419||| 1420||| 1421||| 1422||| 1423||| 1424||| 1425||| 1426||| 1427||| 1428||| 1429||| 1430||| 1431||| 1432||| 1433||| 1434||| 1435||| 1436||| 1437||| 1438||| 1439||| 1440||| 1441||| 1442||| 1443||| 1444||| 1445||| 1446||| 1447||| 1448||| 1449||| 1450||| 1451||| 1452||| 1453||| 1454||| 1455||| 1456||| 1457||| 1458||| 1459||| 1460||| 1461||| 1462||| 1463||| 1464||| 1465||| 1466||| 1467||| 1468||| 1469||| 1470||| 1471||| 1472||| 1473||| 1474||| 1475||| 1476||| 1477||| 1478||| 1479||| 1480||| 1481||| 1482||| 1483||| 1484||| 1485||| 1486||| 1487||| 1488||| 1489||| 1490||| 1491||| 1492||| 1493||| 1494||| 1495||| 1496||| 1497||| 1498||| 1499||| 1500||| 1501||| 1502||| 1503||| 1504||| 1505||| 1506||| 1507||| 1508||| 1509||| 1510||| 1511||| 1512||| 1513||| 1514||| 1515||| 1516||| 1517||| 1518||| 1519||| 1520||| 1521||| 1522||| 1523||| 1524||| 1525||| 1526||| 1527||| 1528||| 1529||| 1530||| 1531||| 1532||| 1533||| 1534||| 1535||| 1536||| 1537||| 1538||| 1539||| 1540||| 1541||| 1542||| 1543||| 1544||| 1545||| 1546||| 1547||| 1548||| 1549||| 1550||| 1551||| 1552||| 1553||| 1554||| 1555||| 1556||| 1557||| 1558||| 1559||| 1560||| 1561||| 1562||| 1563||| 1564||| 1565||| 1566||| 1567||| 1568||| 1569||| 1570||| 1571||| 1572||| 1573||| 1574||| 1575||| 1576||| 1577||| 1578||| 1579||| 1580||| 1581||| 1582||| 1583||| 1584||| 1585||| 1586||| 1587||| 1588||| 1589||| 1590||| 1591||| 1592||| 1593||| 1594||| 1595||| 1596||| 1597||| 1598||| 1599||| 1600||| 1601||| 1602||| 1603||| 1604||| 1605||| 1606||| 1607||| 1608||| 1609||| 1610||| 1611||| 1612||| 1613||| 1614||| 1615||| 1616||| 1617||| 1618||| 1619||| 1620||| 1621||| 1622||| 1623||| 1624||| 1625||| 1626||| 1627||| 1628||| 1629||| 1630||| 1631||| 1632||| 1633||| 1634||| 1635||| 1636||| 1637||| 1638||| 1639||| 1640||| 1641||| 1642||| 1643||| 1644||| 1645||| 1646||| 1647||| 1648||| 1649||| 1650||| 1651||| 1652||| 1653||| 1654||| 1655||| 1656||| 1657||| 1658||| 1659||| 1660||| 1661||| 1662||| 1663||| 1664||| 1665||| 1666||| 1667||| 1668||| 1669||| 1670||| 1671||| 1672||| 1673||| 1674||| 1675||| 1676||| 1677||| 1678||| 1679||| 1680||| 1681||| 1682||| 1683||| 1684||| 1685||| 1686||| 1687||| 1688||| 1689||| 1690||| 1691||| 1692||| 1693||| 1694||| 1695||| 1696||| 1697||| 1698||| 1699||| 1700||| 1701||| 1702||| 1703||| 1704||| 1705||| 1706||| 1707||| 1708||| 1709||| 1710||| 1711||| 1712||| 1713||| 1714||| 1715||| 1716||| 1717||| 1718||| 1719||| 1720||| 1721||| 1722||| 1723||| 1724||| 1725||| 1726||| 1727||| 1728||| 1729||| 1730||| 1731||| 1732||| 1733||| 1734||| 1735||| 1736||| 1737||| 1738||| 1739||| 1740||| 1741||| 1742||| 1743||| 1744||| 1745||| 1746||| 1747||| 1748||| 1749||| 1750||| 1751||| 1752||| 1753||| 1754||| 1755||| 1756||| 1757||| 1758||| 1759||| 1760||| 1761||| 1762||| 1763||| 1764||| 1765||| 1766||| 1767||| 1768||| 1769||| 1770||| 1771||| 1772||| 1773||| 1774||| 1775||| 1776||| 1777||| 1778||| 1779||| 1780||| 1781||| 1782||| 1783||| 1784||| 1785||| 1786||| 1787||| 1788||| 1789||| 1790||| 1791||| 1792||| 1793||| 1794||| 1795||| 1796||| 1797||| 1798||| 1799||| 1800||| 1801||| 1802||| 1803||| 1804||| 1805||| 1806||| 1807||| 1808||| 1809||| 1810||| 1811||| 1812||| 1813||| 1814||| 1815||| 1816||| 1817||| 1818||| 1819||| 1820||| 1821||| 1822||| 1823||| 1824||| 1825||| 1826||| 1827||| 1828||| 1829||| 1830||| 1831||| 1832||| 1833||| 1834||| 1835||| 1836||| 1837||| 1838||| 1839||| 1840||| 1841||| 1842||| 1843||| 1844||| 1845||| 1846||| 1847||| 1848||| 1849||| 1850||| 1851||| 1852||| 1853||| 1854||| 1855||| 1856||| 1857||| 1858||| 1859||| 1860||| 1861||| 1862||| 1863||| 1864||| 1865||| 1866||| 1867||| 1868||| 1869||| 1870||| 1871||| 1872||| 1873||| 1874||| 1875||| 1876||| 1877||| 1878||| 1879||| 1880||| 1881||| 1882||| 1883||| 1884||| 1885||| 1886||| 1887||| 1888||| 1889||| 1890||| 1891||| 1892||| 1893||| 1894||| 1895||| 1896||| 1897||| 1898||| 1899||| 1900||| 1901||| 1902||| 1903||| 1904||| 1905||| 1906||| 1907||| 1908||| 1909||| 1910||| 1911||| 1912||| 1913||| 1914||| 1915||| 1916||| 1917||| 1918||| 1919||| 1920||| 1921||| 1922||| 1923||| 1924||| 1925||| 1926||| 1927||| 1928||| 1929||| 1930||| 1931||| 1932||| 1933||| 1934||| 1935||| 1936||| 1937||| 1938||| 1939||| 1940||| 1941||| 1942||| 1943||| 1944||| 1945||| 1946||| 1947||| 1948||| 1949||| 1950||| 1951||| 1952||| 1953||| 1954||| 1955||| 1956||| 1957||| 1958||| 1959||| 1960||| 1961||| 1962||| 1963||| 1964||| 1965||| 1966||| 1967||| 1968||| 1969||| 1970||| 1971||| 1972||| 1973||| 1974||| 1975||| 1976||| 1977||| 1978||| 1979||| 1980||| 1981||| 1982||| 1983||| 1984||| 1985||| 1986||| 1987||| 1988||| 1989||| 1990||| 1991||| 1992||| 1993||| 1994||| 1995||| 1996||| 1997||| 1998||| 1999||| 19900|||  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/225, 951  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5985589and, Greta E.  
 REGISTRATION NUMBER: 35, 302  
 REFERENCE/DOCKET NUMBER: 27866/33441  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 INFORMATION FOR SEQ ID NO: 11:  
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 STRANDEDNESS: single  
 TYPE: nucleic acid  
 TOPOLogy: linear  
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 US-09-225-951-11  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 Strands 1  
 Qy 1149 ccctggaggccgcgtcccgatc 1171  
 Db 23 CCCTGGAGCACCCGTCGGCATC 1  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 Strands 1  
 Qy 1150 ||||||| 1151||| 1152||| 1153||| 1154||| 1155||| 1156||| 1157||| 1158||| 1159||| 1160||| 1161||| 1162||| 1163||| 1164||| 1165||| 1166||| 1167||| 1168||| 1169||| 1170||| 1171||| 1172||| 1173||| 1174||| 1175||| 1176||| 1177||| 1178||| 1179||| 1180||| 1181||| 1182||| 1183||| 1184||| 1185||| 1186||| 1187||| 1188||| 1189||| 1190||| 1191||| 1192||| 1193||| 1194||| 1195||| 1196||| 1197||| 1198||| 1199||| 1100||| 1101||| 1102||| 1103||| 1104||| 1105||| 1106||| 1107||| 1108||| 1109||| 1110||| 1111||| 1112||| 1113||| 1114||| 1115||| 1116||| 1117||| 1118||| 1119||| 11100||| 11101||| 11102||| 11103||| 11104||| 11105||| 11106||| 11107||| 11108||| 11109||| 11110||| 11111||| 11112||| 11113||| 11114||| 11115||| 11116||| 11117||| 11118||| 11119||| 11120||| 11121||| 11122||| 11123||| 11124||| 11125||| 11126||| 11127||| 11128||| 11129||| 11130||| 11131||| 11132||| 11133||| 11134||| 11135||| 11136||| 11137||| 11138||| 11139||| 11140||| 11141||| 11142||| 11143||| 11144||| 11145||| 11146||| 11147||| 11148||| 11149||| 11150||| 11151||| 11152||| 11153||| 11154||| 11155||| 11156||| 11157||| 11158||| 11159||| 11160||| 11161||| 11162||| 11163||| 11164||| 11165||| 11166||| 11167||| 11168||| 11169||| 11170||| 11171||| 11172||| 11173||| 11174||| 11175||| 11176||| 11177||| 11178||| 11179||| 11180||| 11181||| 11182||| 11183||| 11184||| 11185||| 11186||| 11187||| 11188||| 11189||| 11190||| 11191||| 11192||| 11193||| 11194||| 11195||| 11196||| 11197||| 11198||| 11199||| 11100||| 11101||| 11102||| 11103||| 11104||| 11105||| 11106||| 11107||| 11108||| 11109||| 11110||| 11111||| 11112||| 11113||| 11114||| 11115||| 11116||| 11117||| 11118||| 11119||| 11120||| 11121||| 11122||| 11123||| 11124||| 11125||| 11126||| 11127||| 11128||| 11129||| 11130||| 11131||| 11132||| 11133||| 11134||| 11135||| 11136||| 11137||| 11138||| 11139||| 11140||| 11141||| 11142||| 11143||| 11144||| 11145||| 11146||| 11147||| 11148||| 11149||| 11150||| 11151||| 11152||| 11153||| 11154||| 11155||| 11156||| 11157||| 11158||| 11159||| 11160||| 11161||| 11162||| 11163||| 11164||| 11165||| 11166||| 11167||| 11168||| 11169||| 11170||| 11171||| 11172||| 11173||| 11174||| 11175||| 11176||| 11177||| 11178||| 11179||| 11180||| 11181||| 11182||| 11183||| 11184||| 11185||| 11186||| 11187||| 11188||| 11189||| 11190||| 11191||| 11192||| 11193||| 11194||| 11195||| 11196||| 11197||| 11198||| 11199||| 11100||| 11101||| 11102||| 11103||| 11104||| 11105||| 11106||| 11107||| 11108||| 11109||| 11110||| 11111||| 11112||| 11113||| 11114||| 11115||| 11116||| 11117||| 11118||| 11119||| 11120||| 11121||| 11122||| 11123||| 11124||| 11125||| 11126||| 11127||| 11128||| 11129||| 11130||| 11131||| 11132||| 11133||| 11134||| 11135||| 11136||| 11137||| 11138||| 11139||| 11140||| 11141||| 11142||| 11143||| 11144||| 11145||| 11146||| 11147||| 11148||| 11149||| 11150||| 11151||| 11152||| 11153||| 11154||| 11155||| 11156||| 11157||| 11158||| 11159||| 11160||| 11161||| 11162||| 11163||| 11164||| 11165||| 11166||| 11167||| 11168||| 11169||| 11170||| 11171||| 11172||| 11173||| 11174||| 11175||| 11176||| 11177||| 11178||| 11179||| 11180||| 11181||| 11182||| 11183||| 11184||| 11185||| 11186||| 11187||| 11188||| 11189||| 11190||| 11191||| 11192||| 11193||| 11194||| 11195||| 11196||| 11197||| 11198||| 11199||| 11100||| 11101||| 11102||| 11103||| 11104||| 11105||| 11106||| 11107||| 11108||| 11109||| 11110||| 11111||| 11112||| 11113||| 11114||| 11115||| 11116||| 11117||| 11118||| 11119||| 11120||| 11121||| 11122||| 11123||| 11124||| 11125||| 11126||| 11127||| 11128||| 11129||| 11130||| 11131||| 11132||| 11133||| 11134||| 11135||| 11136||| 11137||| 11138||| 11139||| 11140||| 11141||| 11142||| 11143||| 11144||| 11145||| 11146||| 11147||| 11148||| 11149||| 11150||| 11151||| 11152||| 11153||| 11154||| 11155||| 11156||| 11157||| 11158||| 11159||| 11160||| 11161||| 11162||| 11163||| 11164||| 11165||| 11166||| 11167||| 11168||| 11169||| 11170||| 11171||| 11172||| 11173||| 11174||| 11175||| 11176||| 11177||| 11178||| 11179||| 11180||| 11181||| 11182||| 11183||| 11184||| 11185||| 11186||| 11187||| 11188||| 11189||| 11190||| 11191||| 11192||| 11193||| 11194||| 11195||| 11196||| 11197||| 11198||| 11199||| 11100||| 11101||| 11102||| 11103||| 11104||| 11105||| 11106|||

; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-09-225-951-12

TOPLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-09-225-951-12

---

APPLICANT: Hoekstra, Merl F.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: No. 5,882,910el Lipid Kinase

CURRRENT ADDRESS:  
 ADDRESS: Marshall O'Toole Gerstein Murray & Borun  
 STREET: 3000 Sears Tower/233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60605  
 COMPUTER READABLE FORM:  
 Query Match 0.6%; Score 23; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 23; Conservative 0; Mismatches 0;  
 Qy 1132 ctctgtgtccctgtggccctgg 1154  
 Db 23 CTCCTGAGTCCCTGGTCCCTGG 1

APPLICATION NUMBER: US/09/225,951

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5085589 and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-09-225-951-14

Query Match Similarity 0.6%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1501 ggaaacctggcccttacatgtgg 1522  
||| ||||| ||||| ||||| |||||  
Db 22 GGAAACGCTGCCCTACATGTGG 1

Search completed: September 7, 2002, 05:24:35  
Job time: 11656 sec

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GenCore version 4.5  
OM nucleic - nucleic search, using sw model

Result No.	Score	Query Match	Length	DB	ID	Description	
						Sequence 9, Appli	Sequence 10, Appli
c	1	26	0.7	26	11	US-08-777-405-9	Sequence 9, Appli
c	2	26	0.7	26	13	US-08-977-811-9	Sequence 9, Appli
c	3	25	0.6	25	11	US-08-777-405-10	Sequence 10, Appli
c	4	25	0.6	25	13	US-08-977-871-10	Sequence 10, Appli
c	5	23	0.6	23	11	US-08-777-405-11	Sequence 11, Appli
c	6	23	0.6	23	11	US-08-777-405-12	Sequence 12, Appli
c	7	23	0.6	23	13	US-08-977-871-11	Sequence 11, Appli
c	8	23	0.6	23	13	US-08-977-871-12	Sequence 12, Appli
c	9	22	0.6	22	11	US-08-777-405-14	Sequence 14, Appli
c	10	22	0.6	22	13	US-08-977-871-14	Sequence 14, Appli
c	11	21	0.6	29	17	US-09-304-232-73	Sequence 73, Appli
c	12	21	0.5	21	1	PCT-US00-00535-3	Sequence 3, Appli
c	13	21	0.5	21	11	US-08-777-405-7	Sequence 7, Appli
c	14	21	0.5	21	11	US-08-777-405-8	Sequence 8, Appli
c	15	21	0.5	21	11	US-08-777-405-16	Sequence 16, Appli
c	16	21	0.5	21	13	US-08-977-871-1	Sequence 7, Appli
c	17	21	0.5	21	13	US-08-977-871-8	Sequence 8, Appli
c	18	21	0.5	21	13	US-08-977-871-16	Sequence 16, Appli
c	19	21	0.5	21	37	US-10-049-743-3	Sequence 3, Appli
c	20	21	0.5	21	74	US-60-350-061-445	Sequence 445, App
c	21	21	0.5	21	74	US-60-350-061-517	Sequence 517, App
c	22	21	0.5	21	74	US-60-350-061-632	Sequence 632, App
c	23	21	0.5	21	74	US-60-350-061-671	Sequence 671, App
c	24	21	0.5	21	74	US-60-350-061-819	Sequence 819, App
c	25	21	0.5	21	74	US-60-350-061-934	Sequence 934, App
c	26	20	0.5	25	74	US-60-353-987-900212	Sequence 900212, App
c	27	20	0.5	35	US-09-545-542784	Sequence 532784, App	
c	28	20	0.5	25	62	US-60-234-017-51404	Sequence 521404, App
c	29	20	0.5	25	74	US-60-353-987-986246	Sequence 796246, App
c	30	20	0.5	1	PCT-US00-00525-8	Sequence 8, Appli	
c	31	20	0.5	1	PCT-US00-00535-9	Sequence 9, Appli	

RESULT 1  
 US-08-777-405-9/c  
 Sequence 9, Application US/08777405  
 GENERAL INFORMATION:  
 APPLICANT: Chantry, David  
 APPLICANT: Hoekstra, Merl F.  
 APPLICANT: Holtzman, Douglas A  
 TITLE OF INVENTION: Novel Lipid Kinase  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
 STREET: 6300 Sears Tower/233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60606  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/977,871  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Noland, Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/33441  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 26 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-977-871-9

RESULT 1  
 US-08-777-405-9/c  
 Sequence 9, Application US/08777405  
 GENERAL INFORMATION:  
 APPLICANT: Chantry, David  
 APPLICANT: Hoekstra, Merl F.  
 APPLICANT: Holtzman, Douglas A  
 TITLE OF INVENTION: Novel Lipid Kinase  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
 STREET: 6300 Sears Tower/233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60606  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/977,871  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Noland, Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/33441  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 26 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-977-871-9

Query Match 0.7%; Score 26; DB 11; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+05; Indels 0; Gaps 0;  
 Matches 26; Conservative 0; Mismatches 0; Gaps 0;

QY 1500 99gaacgtggcttacatgtggcc 1525  
 Db 26 GGAACCTGGCTTACATGAGGCC 1

RESULT 3  
 US-08-777-405-10/c  
 Sequence 10, Application US/08777405  
 GENERAL INFORMATION:  
 APPLICANT: Chantry, David  
 APPLICANT: Hoekstra, Merl F.  
 APPLICANT: Holtzman, Douglas A  
 TITLE OF INVENTION: Novel Lipid Kinase  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
 STREET: 6300 Sears Tower/233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60606  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/977,871

RESULT 2  
 US-08-977-871-9/c  
 Query Match 0.7%; Score 26; DB 11; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+05; Indels 0; Gaps 0;  
 Matches 26; Conservative 0; Mismatches 0; Gaps 0;  
 QY 1500 99gaacgtggcttacatgtggcc 1525  
 Db 26 GGAACCTGGCTTACATGAGGCC 1

FILING DATE: Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E. REFERENCE/DOCKET NUMBER: 35, 302

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

US-08-777-405-10

Query Match 0.6%; Score 25; DB 11; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1435 ggccgactggccatgtggcc 1459  
Db 25 GGCGACTGCCATGGCTGGCC 1

RESULT 4

US-08-977-871-10/C Sequence 10, Application US/08977871

GENERAL INFORMATION:  
APPLICANT: Chantry, David  
APPLICANT: Hoekstra, Merl F.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: Novel Lipid Kinase  
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6300 Sears Tower/233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777, 405  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REFERENCE/DOCKET NUMBER: 35, 302

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

US-08-777-405-11

Query Match 0.6%; Score 23; DB 11; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ccctggagcgcgttccatc 1171  
Db 23 CCCTGAGACCCGTTCCGCATC 1

RESULT 6

US-08-777-405-12/C Sequence 12, Application US/08777405

GENERAL INFORMATION:  
APPLICANT: Chantry, David  
APPLICANT: Hoekstra, Merl F.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: Novel Lipid Kinase  
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6300 Sears Tower/233 South Wacker Drive  
CITY: Chicago

Query Match 0.6%; Score 25; DB 13; Length 25;





CURRENT APPLICATION NUMBER: PCT/US00/00525  
 CURRENT FILING DATE: 2000-01-06  
 ; EARLIER APPLICATION NUMBER: US 09/357,070  
 ; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 3  
 LENGTH: 21  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: PCR Primer

PCT-US00-00525-3  
 Query Match Similarity 0.5%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+06; Mismatches 0;  
 Matches 21; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
 QY 357 agtatacgcccttcacaca 377  
 Db 21 AGTATGAGCCGCCTTCACCA 1

RESULT 13

US-08-777-405-7  
 Sequence 7, Application US/08777405

GENERAL INFORMATION:

APPLICANT: Chantry, David  
 APPLICANT: Hoekstra, Merl F.  
 APPLICANT: Holtzman, Douglas A.  
 TITLE OF INVENTION: Novel Lipid Kinase  
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray &amp; Borun

STREET: 6300 Sears Tower/233 South Wacker Drive

CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777,405

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6500

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base Pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-777-405-8

Query Match Similarity 0.5%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3e+06; Mismatches 0;  
 Matches 21; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 2899 ccgagagatgggcaggttt 2919

Db 21 CCGAGAGAGTGGCAGCTGTT 1

Query Match Similarity 0.5%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3e+06; Mismatches 0;  
 Matches 21; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 2557 catgtcgaccctgtcgatgt 2577

Db 1 CATGCTGACCCCTGAGATGT 21

RESULT 14

US-08-777-405-8/C  
 Sequence 8, Application US/08777405

GENERAL INFORMATION:

APPLICANT: Chantry, David  
 APPLICANT: Hoekstra, Merl F.  
 APPLICANT: Holtzman, Douglas A.  
 TITLE OF INVENTION: Novel Lipid Kinase  
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray &amp; Borun

STREET: 6300 Sears Tower/233 South Wacker Drive

CITY: Chicago  
 STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777,405

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6500

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base Pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-777-405-8

Query Match Similarity 0.5%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3e+06; Mismatches 0;  
 Matches 21; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 2899 ccgagagatgggcaggttt 2919

Db 21 CCGAGAGAGTGGCAGCTGTT 1

Query Match Similarity 0.5%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3e+06; Mismatches 0;  
 Matches 21; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 2557 catgtcgaccctgtcgatgt 2577

Db 1 CATGCTGACCCCTGAGATGT 21

Query Match Similarity 0.5%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+06; Mismatches 0;  
 Matches 21; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 2557 catgtcgaccctgtcgatgt 2577

Db 1 CATGCTGACCCCTGAGATGT 21

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,405  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-777-405-16

Query Match 0.5%; Score 21; DB 11; Length 21;  
Best Local Similarity 100.0%; Pred. No. 6.3e+06;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db |||||||  
21 tcacaaggcaacatggcag 1

Search completed: September 7, 2002, 06:48:39  
Job time: 12644 sec

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GenCore version 4.5

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 (without alignments)

total number of hits satisfying chosen parameters: 888728

minimum DB seq length: 0

maximum DB seq length: 30

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : Pending\_Patents\_NA\_New:\*

1: /rcgn2\_6/ptodata/2/pna/us01\_new\_comb.seq:\*

2: /rcgn2\_6/ptodata/2/pna/us01\_new\_comb.seq:\*

3: /rcgn2\_6/ptodata/2/pna/us08\_new\_comb.seq:\*

4: /rcgn2\_6/ptodata/2/pna/us08\_new\_comb.seq:\*

5: /rcgn2\_6/ptodata/2/pna/us10\_new\_comb.seq:\*

6: /rcgn2\_6/ptodata/2/pna/us10\_new\_comb.seq:\*

7: /rcgn2\_6/ptodata/2/pna/us10\_new\_comb.seq:\*

8: /rcgn2\_6/ptodata/2/pna/us60\_NEW\_COMBO.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

result NO.	Score	Query Match Length	DB ID	Description
1	19.8	0.5	25	US-09-396-196G-11682
2	18.8	0.5	25	US-09-396-196G-47365
3	18.8	0.5	25	US-09-396-196G-127145
4	18.8	0.5	30	US-09-396-196G-127145
5	18.6	0.5	25	US-09-396-604-110238
6	18.6	0.5	25	US-09-396-520431
7	18.2	0.5	25	US-09-396-196G-2283
8	18.2	0.5	25	US-09-396-196G-47366
9	18.0	0.5	30	US-10-09-171-3
10	17.8	0.5	22	US-09-544-398A-203
11	17.8	0.5	22	US-09-544-398B-203
12	17.8	0.5	25	US-09-546-2242
13	17.8	0.5	25	US-09-396-196G-44655
14	17.8	0.5	25	US-09-396-196G-10223
15	17.6	0.5	25	US-09-956-604-81730
16	17.6	0.5	25	US-09-956-604-9053
17	17.6	0.5	25	US-09-396-196G-11131
18	17.6	0.5	25	US-09-396-196G-11681
19	17.6	0.5	25	US-09-396-196G-66133
20	17.6	0.5	25	US-09-396-196G-67635
21	17.6	0.5	25	US-09-396-196G-70513
22	17.6	0.5	25	US-09-396-196G-70513
23	17.6	0.5	25	US-09-396-196G-84193
24	17.6	0.5	25	US-09-396-196G-95477
25	17.6	0.5	25	US-09-396-196G-114370

**ALIGNMENTS**

RESULT 1

US-09-396-196G-11682

; Sequence 11682, Application US/09396196G

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127805

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 11682

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

; US-09-396-196G-11682

RESULT 2

US-09-396-196G-47365

; Sequence 47365, Application US/09396196G

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127805

; SOFTWARE: FastSEQ for Windows Version 4.0

Sequence	251,	App
Sequence	51106,	A
Sequence	51119,	A
Sequence	40760,	A
Sequence	42255,	A
Sequence	42272,	A
Sequence	8,	Appl
Sequence	5847,	AP
Sequence	124611,	
Sequence	124574,	
Sequence	9391,	AP
Sequence	14744,	A
Sequence	34452,	A
Sequence	49850,	A
Sequence	71621,	A
Sequence	77991,	A
Sequence	95478,	A
Sequence	115095,	A

```

; SEQ ID NO: 47365
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-47365

Query Match          0. 5%; Score 18. 8; DB 5; Length 25;
Best Local Similarity 90. 9%; Pred. No. 1. 8e+06; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 2; DB 3 ctgcctatcgccgtggcggg 24

RESULT 3
US-09-396-196G-127145
; Sequence 127145, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO 127145
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-127145

RESULT 4
US-09-380-447A-137
; Sequence 137, Application US/09380447A
; GENERAL INFORMATION:
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Weiss, Gregory A.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: IMPROVEMENTS IN PHAGE DISPLAY
; FILE REFERENCE: P1581R2
; CURRENT APPLICATION NUMBER: US/09/380,447A
; CURRENT FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 60/134,870
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/133,296
; PRIOR FILING DATE: 1999-05-10
; PRIOR APPLICATION NUMBER: US 60/103,514
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/094,291
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: PCT/USUS99/16596
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 287
; SEQ ID NO 137
; LENGTH: 30
; TYPE: DNA

Query Match          0. 5%; Score 18. 8; DB 5; Length 30;
Best Local Similarity 76. 7%; Pred. No. 1. 8e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 7; DB 1 cgcgcgaatgtgcacaatctcgaggag 643
; OTHER INFORMATION: linker oligonucleotide
; US-09-380-447A-137

RESULT 5
US-09-956-604-110238
; Sequence 110238, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO 110238
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-956-604-110238

RESULT 6
US-09-396-196G-52841
; Sequence 52841, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO 52841
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-52841

Query Match          0. 5%; Score 18. 6; DB 5; Length 25;
Best Local Similarity 84. 0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 4; DB 1 ctggccctgaggcgccggc 3151
; OTHER INFORMATION: artificial sequence
; FEATURE: linker oligonucleotide
; US-09-380-447A-137

```

```

RESULT 7
; Sequence 3, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 22583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: MUS musculus
; US-09-396-196G-22583

RESULT 8
Query Match 0.5%; Score 18.2; DB 5; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.4e+06; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1983 ccatcaatcgctggaaactg 2005
Db 24 CCATCAAGTCCCTGTGAACTG 2

RESULT 9
Query Match 0.5%; Score 18.2; DB 5; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.4e+06; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1608 tgctcatcgctggccagggtg 1630
Db 1 tgctcatcgccgtcgaggag 23

RESULT 10
Query Match 0.5%; Score 18; DB 6; Length 30;
Best Local Similarity 80.8%; Pred. No. 2.6e+06; Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1419 agaaaaatccaaaggcggactgc 1444
Db 5 agaaaactccaccaaaggcggactgc 30

RESULT 11
Query Match 0.5%; Score 18; DB 6; Length 30;
Best Local Similarity 90.5%; Pred. No. 2.8e+06; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 103 acaatcttaatctggccaggc 123
Db 1 acaatcttaatctggccaggc 21

```

```

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 6/100,678
; PRIORITY FILING DATE: 1998-09-17
; PRIORITY SEQ ID NOS: 127806
; PRIORITY FILING DATE: 1998-01-13
; PRIORITY APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIORITY APPLICATION NUMBER: US 09/229,319
; PRIORITY FILING DATE: 1999-01-13
; PRIORITY APPLICATION NUMBER: US 60/071,449
; PRIORITY FILING DATE: 1998-01-13
; PRIORITY APPLICATION NUMBER: US/09/544,398B
; PRIORITY FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-544-398B-203

Query Match          0.5%; Score 17.8; DB 5; Length 22;
Best Local Similarity 90.5%; Pred. No. 2.8e+06; 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; ; SEQ ID NO 44645
Qy 103 agcatttttaatctccggc 123
Db 1 agcacttttaatgttgtcaagc 21

RESULT 12
US-09-396-196G-22842/c
; Sequence 22842, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIORITY NUMBER: 6/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 22842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-22842

Query Match          0.5%; Score 17.8; DB 5; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+06; 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; ; SEQ ID NO 102323
Qy 1277 tcggaggtagcggtgtcg 1297
Db 23 TCAGAGGTGAGCTTGTCG 3

RESULT 14
US-09-396-196G-102323
; Sequence 102323, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 6/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 102323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-102323

Query Match          0.5%; Score 17.8; DB 5; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+06; 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; ; SEQ ID NO 81730
Qy 1849 ggtcaccaaatgggacaaga 1869
Db 2 ggtcaccatgggacaaga 22

RESULT 15
US-09-956-604-81730
; Sequence 81730, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIORITY NUMBER: 6/0/234,049
; PRIORITY FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141639
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81730
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-956-604-81730

Query Match          0.5%; Score 17.8; DB 5; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.8e+06; 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; ; SEQ ID NO 81730
Qy 3779 tctggaaatccccaggc 3799
Db 22 TCTGGCTGATCCCCGAGGC 2

RESULT 13
US-09-396-196G-44645/c
; Sequence 44645, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIORITY NUMBER: 6/0/234,049
; PRIORITY FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141639
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81730
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-956-604-81730

```

Query Match 0.5%; Score 17.6; DB 5; Length 25;  
Best Local Similarity 83.3%; Pred. No. 3.1e+06;  
Matches 20; Conservative 0; Mismatches 4; Indels 0;  
Gaps 0;

Qy 2972 acccgcgacgtgcattcattc 2995  
|||||| |||||| |||||  
Db 1 acccgagacatgttccaaatttcattc 24

Search completed: September 7, 2002, 06:59:45  
Job time: 10465 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model.  
Run on: September 7, 2002, 02:03:24 ; Search time 2817.9 Seconds  
(without alignments)  
18526.641 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattccggcacgaggcg... ... ggttttgggtacgagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapext 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 28088

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb.est1:\*
- 10: gb.est2:\*
- 11: gb\_htc:\*
- 12: gb\_gss:\*
- 13: em\_gss\_hum:\*
- 14: em\_gss\_inv:\*
- 15: em\_gss\_pln:\*
- 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	ALIGNMENTS
1	19.6	0.5	28	10	T47368	T47368	1	RESULT	
2	18.6	0.5	30	10	BM399411	BM399411	5005-0-57	LOCUS	
3	18.0	0.5	28	9	AL584657	AL584657	AL584657	DEFINITION	IMAGE:31023 5' similar to simila
4	16.8	0.4	26	12	A2419681	A2419681	IM0300G02	PROTEIN	r1 Strategene placenta (#937225) Homo sapiens cDNA clone FIBROBLAST ISOFORM (HUMAN), mRNA sequence.
5	16.8	0.4	26	12	A2780072	A2780072	2M017H04	ACCESSION	T47368
6	16.8	0.4	26	12	A2780802	A2780802	2M0018F24	VERSION	T47368.1 GI:649349
7	16.8	0.4	26	12	A282508	A282508	2M009P18	KEYWORDS	EST.
8	16.8	0.4	26	12	A284682	A284682	2M0027B07	SOURCE	human.
9	16.8	0.4	26	12	A2942905	A2942905	2M0203K13	ORGANISM	Homo sapiens
10	16.6	0.4	27	12	A2942945	A2942945	A1625245 ts4z4e52	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; I (bases 1 to 28)
11	16.4	0.4	27	12	A308059	A308059	A1697335 tq18a01.X	AUTHORS	Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Len, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Relfkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Woldmann, P., Waterston, R., Wilson, R., and Marr, M.
12	16.4	0.4	29	12	A3091936	A3091936	A1756191 ETESTea40	COMMENT	Generation and analysis of 280,000 human expressed sequence tags
13	16.2	0.4	22	9	AA953755	AA953755	on9903.S	JOURNAL	Genome Res. 6 (9), 807-828 (1996)
14	16.2	0.4	30	10	AA959127	AA959127	BM99817 5009-0-41	MEDLINE	97044478
15	16.0	0.4	30	12	A2343274	A2343274	IM0076C04	COMMENT	Contact: Wilson RK
16	16.0	0.4	30	12	A2601864	A2601864	IM0120P16	COMMENT	Washington University School of Medicine
17	16.0	0.4	25	9	AA766400	AA766400	IM03603.S	COMMENT	4444 Forest Park Parkway, Box 8301, St. Louis, MO 63108
18	16.0	0.4	30	12	A212603P	A212603P	AL479776 T. brucei	COMMENT	Tel: 314 286 1800 Fax: 314 286 1100 Email: est@wustl.edu
19	16.0	0.4	30	12	AZ371129	AZ371129	IM0122M02	COMMENT	Insert Size: 89
20	15.8	0.4	28	9	A933742	A933742	A2343274 om5ch09.S	COMMENT	High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace sequence considered overall poor quality
21	15.8	0.4	28	12	A2245640	A2245640	AZ33742 om5ch09.S	COMMENT	Insert Length: 89 Std Error: 0.00
22	15.8	0.4	28	12	A2502451	A2502451	A2502451 IM0341D17	COMMENT	Seq primer: M13RPI
23	15.6	0.4	27	10	D45117	D45117	DA5817 HUMG03036	COMMENT	High quality sequence stop: 1 Location/Qualifiers
24	15.8	0.4	29	10	AV85654	AV85654	AV82654 AV82654	COMMENT	Location/Qualifiers
25	15.8	0.4	30	9	A2416559	A2416559	A2476559 1M039C02	COMMENT	Location/Qualifiers
26	15.8	0.4	29	12	A2308159	A2308159	A2308159 1M010N09	COMMENT	Location/Qualifiers
27	15.6	0.4	24	12	A235323	A235323	A235323 1M0079M16	COMMENT	Location/Qualifiers
28	15.6	0.4	24	12	A240206	A240206	A240206 1M0172I20	COMMENT	Location/Qualifiers
29	15.6	0.4	28	9	A1003112	A1003112	A1003112 ua7a03.r	COMMENT	Location/Qualifiers
30	15.6	0.4	29	12	A2803680	A2803680	A2803680 2M0064009	COMMENT	Location/Qualifiers
31	15.6	0.4	30	12	A2780802	A2780802	A2780802 2M0018F24	COMMENT	Location/Qualifiers
32	15.4	0.4	30	12	A282508	A282508	A282508 2M009P18	COMMENT	Location/Qualifiers
33	15.4	0.4	20	12	A2784682	A2784682	A2784682 2M0027B07	COMMENT	Location/Qualifiers
34	15.4	0.4	22	12	A2942905	A2942905	A2942905 2M0203K13	COMMENT	Location/Qualifiers
35	15.4	0.4	28	9	A1625245	A1625245	A1625245 tsq18a01.X	COMMENT	Location/Qualifiers
36	15.4	0.4	29	12	A2803680	A2803680	A2803680 2M0064009	COMMENT	Location/Qualifiers
37	15.4	0.4	30	12	A2780802	A2780802	A2780802 2M0018F24	COMMENT	Location/Qualifiers
38	15.2	0.4	30	12	A282508	A282508	A282508 2M009P18	COMMENT	Location/Qualifiers
39	15.2	0.4	20	12	A2784682	A2784682	A2784682 2M0027B07	COMMENT	Location/Qualifiers
40	15.2	0.4	22	12	A2942905	A2942905	A2942905 2M0203K13	COMMENT	Location/Qualifiers
41	15.2	0.4	28	9	A1697335	A1697335	A1697335 tq18a01.X	COMMENT	Location/Qualifiers
42	15.2	0.4	28	9	A1756191	A1756191	A1756191 ETESTea40	COMMENT	Location/Qualifiers
43	15.2	0.4	28	9	A2591936	A2591936	A2591936 1M0402N20	COMMENT	Location/Qualifiers
44	15.2	0.4	28	12	AZ591954	AZ591954	AZ591954 1M0402N20	COMMENT	Location/Qualifiers
45	15.2	0.4	28	12	AZ591954	AZ591954	AZ591954 1M0402N20	COMMENT	Location/Qualifiers

organism="Homo sapiens"  
 /db-xref="GDB:491920"  
 /db-xref="taxon:9606"  
 /clone="IMAGE:71023"  
 /clone-lib="Stratagene placenta (#937225)"  
 /sex="male"  
 /lab host="SOLR cells (kanamycin resistant)"  
 /note="Organ: placenta; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: Xhol; Cloned unidirectionally. Primer:  
 Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP  
 XR Vector; 5' adaptor sequence: 5' GAATTCGCCAGG 3'  
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTT 3'"

\* BASE COUNT 4 a 7 c 11 g 6 t  
 ORIGIN

Query Match	Score	DB	Length	EST
Best Local Similarity	0.5%	10;	28;	28-FEB-2001
Matches	84.6%;	Pred. No.	4.e+06;	
Oy	1204	Mismatches	4;	
Db	2	Indels	0;	
		Gaps	0;	

RESULT 2  
 BM399411 LOCUS BM399411 30 bp mRNA linear EST 17-JAN-2002  
 DEFINITION 5099-0-57-E01.t1 Chilcoat/Turkewitz cDNA (large fraction)  
 Tetrhydmena thermophila CDNA, mRNA sequence.  
 ACCESSION BM399411  
 VERSION BM399411.1 GI:18199464  
 KEYWORDS EST.  
 SOURCE Tetrahymena thermophila.  
 ORGANISM Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
 Hymenostomatida; Tetrahymenina; Tetrahymena.  
 REFERENCE 1 (bases 1 to 30)  
 AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Oris, E., Kirk,K.E., Frankel  
 ,J. and Kloibacher,L.  
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Turkewitz AP  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.

FEATURES source  
 1. .28  
 /organism="Gallus gallus"  
 /db-xref="taxon:9031"  
 /clone="ROS012G12"  
 /clone-lib="stratagene Chick Embryo Lambda cDNA Library (\*  
 93405)"  
 /tissue-type="Embryo"  
 /dev-stage="5 days old"  
 /lab host="SOLR cells (kanamycin resistant)"  
 /note="Vector: pBlUESCRIPT SK; Site\_1: EcoRI; Site\_2: Xhol  
 ; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR  
 vector. Average insert size: 1.5kb.; 5' adaptor sequence: 5'  
 5' GAATTCGCCAGG 3'; 3' adaptor sequence: 5'  
 CTCGAGTTTTTTTTTTT 3'"

BASE COUNT 8 a 7 c 11 g 2 t  
 ORIGIN

Query Match	Score	DB	Length	EST
Best Local Similarity	0.5%	9;	28;	28-FEB-2001
Matches	80.0%;	Pred. No.	9.7e+06;	
Oy	1	Mismatches	0;	
Db	1	Indels	0;	
		Gaps	0;	

RESULT 4  
 A2479681/C LOCUS A2479681 26 bp DNA linear GSS 04-oct-2000  
 DEFINITION 1M03002R Mouse 10kb plasmid TUGC1M library Mus musculus genomic  
 clone UUGC1M0300G2 R, DNA sequence.  
 ACCESSION A2479681  
 VERSION A2479681.1 GI:10639845  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 26)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacon,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederauer,A.,  
 and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss

RESULT 3  
 RESULT

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0300 row: G column: 02

Seq primer: CACAGAGAACAGCTAAGACC  
Class: Plasmid ends

High quality sequence stop: 26.  
Location/Qualifiers

FEATURES  
source  
1. .26  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/lab\_xref="taxon:10090"  
/clone="UUGC1M030G02"  
/clone.lib="Mouse 10kb plasmid UGGC1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
ORIGIN  
13 a 0 c 13 g 0 t

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0017 row: H column: 04

Seq primer: CGTGTAAACGACGCCAGT  
Class: Plasmid ends

High quality sequence stop: 26.  
Location/Qualifiers

FEATURES  
source  
1. .26  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/lab\_xref="taxon:10090"  
/clone="UUGC2M0017H04"  
/clone.lib="Mouse 10kb Plasmid UGGC1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
ORIGIN  
8 a 6 c 8 a 6 c 6 g 6 t

Query Match 0.4%; Score 16 8; DB 12; Length 26;  
Best Local Similarity 90.0%; Pred. No. 1.6e+07; Mismatches 18; Conservatve 0; Indels 0; Gaps 0;

QY 3110 ctccatccctccaccctt 3129  
Db 26 CTCCTCCCTCCCTCTT 7

RESULT 5  
AZ780072 LOCUS AZ780072 26 bp DNA linear GSS 16-FEB-2001  
DEFINITION Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC2M0017H04 F, DNA sequence.

ACCESSION AZ780072  
VERSION AZ780072.1  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0017 row: H column: 04

Seq primer: CGTGTAAACGACGCCAGT  
Class: Plasmid ends

High quality sequence stop: 26.  
Location/Qualifiers

FEATURES  
source  
1. .26  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/lab\_xref="taxon:10090"  
/clone="UUGC2M0017H04"  
/clone.lib="Mouse 10kb Plasmid UGGC1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
ORIGIN  
8 a 6 c 8 a 6 c 6 g 6 t

Query Match 0.4%; Score 16 8; DB 12; Length 26;  
Best Local Similarity 90.0%; Pred. No. 1.6e+07; Mismatches 18; Conservatve 0; Indels 0; Gaps 0;

QY 2851 cacatatgtgcggccatg 2870  
Db 1 CACATATGCCCTGGGATG 20

RESULT 6  
AA973948/C LOCUS AA973948 28 bp mRNA linear EST 23-JUL-1998  
DEFINITION oq12802.s1 NCL\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE:1586115 3', similar to TR:035787\_035787 KINESIN-RELATED PROTEIN.; mRNA sequence.

ACCESSION AA973948  
VERSION AA973948.1  
KEYWORDS EST.

REFERENCE 1 (bases 1 to 26)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Inserts  
JOURNAL Unpublished (1997)

COMMENT  
Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskalkuk, M.D., Ph.D., Michael  
 Bennett-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
<http://www-bio.llnl.gov/bbrp/image/image.html>

Trace considered overall poor quality  
 Insert Length: 790 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.

Location/Qualifiers

FEATURES source

1. .28  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1586115"  
 /clone\_libr="NCI\_CGAP\_Gc4"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DILIB0"  
 /note="Vector: pT7TD-Bac (Pharmacia) with a modified  
 polylinker; 1st strand cDNA was prepared from 3 pooled  
 germ cell tumors, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT7TD  
 vector. Library is normalized. Library was constructed by  
 Bento Soares and M. Fatima Bonaldo."

BASE COUNT ORIGIN

6 a 3 c 11 g 8 t

Query Match 0.4%; Score 16.8; DB 9; Length 30;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+07;  
 Matches 21; Conservative 0; Mismatches 7;  
 Indels 0; Gaps 0;

Qy 3164 agcttctccaaagacatcccgatctcca 3191  
 Db 28 ACCCTCTACATTGACATCCAGGACCTCA 1

RESULT 7

BM398517 LOCUS BM398517 30 bp mRNA linear EST 17-JAN-2002  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
 ACCESSION BM398517  
 VERSION BM398517.1 GI:18198570  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Tetrahymena thermophila.

Best Local Similarity 75.0%; Pred. No. 1.6e+07;  
 Matches 21; Conservative 0; Mismatches 7;  
 Indels 0; Gaps 0;

Query Match 0.4%; Score 16.8; DB 9; Length 28;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+07;  
 Matches 21; Conservative 0; Mismatches 7;  
 Indels 0; Gaps 0;

Qy 3164 agcttctccaaagacatcccgatctcca 3191  
 Db 28 ACCCTCTACATTGACATCCAGGACCTCA 1

RESULT 8

AZ404206 LOCUS AZ404206 27 bp DNA linear GSS 03-OCT-2000  
 DEFINITION IM0172120F Mouse 10kb plasmid UGGCIM library Mus musculus genomic  
 clone UGGCIM0172120 F, DNA sequence.

ACCESSION AZ404206  
 VERSION AZ404206.1 GI:10528219  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 1 (bases 1 to 27)  
 Dunn,D., Avogari,A., Barber,M., Beacorn,T., Duvall,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.

REFERENCE AUTHORS  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Unpublished (2000)

COMMENT JOURNAL  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0172; row: I column: 20  
 Seq primer: CGTTTAAACGACGCCAGT  
 Class: Plasmid ends

High quality sequence stop: 27.  
 Location/Qualifiers

FEATURES source

1. .27  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10240"  
 /clone="UGGCIM0172120"  
 /clone\_libr="Mouse 10kb plasmid UGGCIM library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold,  $\lambda$ -resistant, F-"  
 /note="Vector: pW02nv; Purified genomic DNA from M.  
 musculus C57Bl/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://wwwjax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapter DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pW42 (914732114gb(AfI29072.1), a copy-number  
 inducible derivative of plasmid RI. The vector was ligated

REFERENCE AUTHORS  
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel  
 ,J. and Kloibacher,J.L.  
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkewitz@midway.uchicago.edu  
 Seq primer: T3  
 Location/Qualifiers  
 1. .30  
 FEATURES source  
 /organism="Tetrahymena thermophila"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"

with adaptors complementary to the insert adaptors and purified. The sheared, adaptered mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL1-Gold (Stratagene) cells and selected for ampicillin resistance.

## BASE COUNT

0 a 9 c 9 g 9 t

## ORIGIN

Query Match 0.4%; Score 16.6; DB 12; Length 27;  
Best Local Similarity 82.6%; Pred. No. 1.8e+07; Mismatches 4;  
Matches 19; Conservative 0; Indels 0; Gaps 0;  
Qy 2030 ctgtcgactgtggcagggtct 2052  
Db 1 CTGCTGCIGCTGCTGCTGCT 23

## RESULT

9

## AZ789420/C

AZ789420

240037J11F

Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC2M037J11 F, DNA sequence.

A2789420

A2789420.1

GI:12930223

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 29)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Plate: 0037 row: J column: 11

Seq primer: CGTTGTAACAGCACGCCAGT

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

I. .29

FEATURES

source

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGGC2M037J11"

/clone\_id="Mouse 10kb plasmid UGGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-

/note="Vector: PWD2nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://wwwjax.org/resources/documents/dnares/).

The DNA

was hydrodynamically sheared by repeated

passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end repaired with T4

DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL1-Gold (Stratagene) cells and selected for ampicillin resistance.

## BASE COUNT

8 a

7 c

6 g

8 t

## ORIGIN

Query Match 0.4%; Score 16.4; DB 12; Length 29;  
Best Local Similarity 76.9%; Pred. No. 2e+07; Mismatches 6;  
Matches 20; Conservative 0; Indels 0; Gaps 0;  
Qy 3249 agtttaacaaaggccctccgtggagac 3274  
Db 26 AGTTAAAGATGCAGTCACAGAGC 1

## RESULT

10

A2840149

A2840149

240136046R

Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC2M0136046 R, DNA sequence.

A2840149

A2840149.1

GI:131010057

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 30)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Plate: 0136 row: M column: 06

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

I. .30

FEATURES

source

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGGC2M013606"

/clone\_id="Mouse 10kb plasmid UGGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-

/note="Vector: PWD2nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://wwwjax.org/resources/documents/dnares/).

The DNA

was hydrodynamically sheared by repeated

passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end repaired with T4

DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative





Email: cgabbs-r@mail.nih.gov  
 Tissue procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 cDNA Library preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LUIN at:  
[www-bio.llnl.gov/bbrp/image/](http://www-bio.llnl.gov/bbrp/image/)

Trace considered overall poor quality  
 Insert length: 345 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.

## FEATURES

## source

1.

.25

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1307068"

/clone\_id="NCI:CGAP:GCBI"

/feature\_type="germinal center B cell"

/lab\_host="DH10B"

/note="Vector: pT7TD-PAC (Pharmacia) with a modified polylinker; Site\_1: Not I; site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD+), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer, [5' -GGTTACCACTGAACTGGGCGCGCCATTTTTTTTTTTT-3']. Double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

5

a

4

c

8

g

8

t

Query Match Similarity Score 16; DB 9; Length 25;  
 Best Local Similarity 0.4%; Pred. No. 2.3e+07;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Qy 3495 ttaaggagctaaacagccataaac 3518  
 ||||| ||||| ||||| ||||| |||||  
 Db 25 ttGTGGCCTAACAGCCACAAAC 2

Search completed: September 7, 2002, 04:05:14  
 Job time: 7310 sec